



## SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS FOR DETECTING  
 HEPATITIS E VIRUS

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<223> Orf3 at positions 5094-5462

<223> Xaa = Unknown or Other at position 174

<223> Xaa = Unknown or Other at position 363

<223> Xaa = Unknown or Other at position 1088

<223> Xaa = Unknown or Other at position 1131

<223> Xaa = Unknown or Other at position 1217

<223> Xaa = Unknown or Other at position 1389

<223> Xaa = Unknown or Other at position 2179

<223> Xaa = Unknown or Other at position 2240

<223> Xaa = Unknown or Other at position 2293

<400> 90

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Pro Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn	
1 5 10 15	
tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tct cgc gtg	96
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val	
20 25 30	
caa acc gag att ctt att aat ttg atg caa ccc cgg cag ttg gtt ttc	144
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cgc cct gag gta ctt tgg aat cac cct atc cag cgg gtt ata cat aat	192
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gaa tta gaa cag tac tgc cgg gct cgg gct ggt cgt tgc ttg gag gtt	240
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75 80	
gga gct cac cca aga tcc att aat gac aac ccc aac gtt ctg cat cgg	288
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
85 90 95	
tgt ttc ctt aga ccg gtt ggc cga gat gtt cag cgc tgg tac tct gcc	336
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc acc cgc ggc cct gcg gct aat tgc cgc cgc tcc gcg ttg cgt ggt	384
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc ccc ccc gct gac cgc act tac tgc ttt gat gga ttc tcc cgt tgt	432
Leu Pro Pro Ala Asp Arg Thr Tyr Cys Phe Asp Gly Phe Ser Arg Cys	
130 135 140	
gct ttt gct gca gag acc ggt gtg gct ctt tac tct ctg cat gac ctt	480
Ala Phe Ala Ala Glu Thr Gly Val Ala Leu Tyr Ser Leu His Asp Leu	
145 150 155 160	
tgg cca gct gat gca gag gct atg gcc cgc cac ggg atr aca cgc	528
Trp Pro Ala Asp Val Ala Glu Ala Met Ala Arg His Gly Xaa Thr Arg	
165 170 175	
ttg tat gcc gca ctg cac ctt ccc cct gag gtg ctg cta cca ccc ggc	576
Leu Tyr Ala Ala Leu His Leu Pro Pro Glu Val Leu Leu Pro Pro Gly	
180 185 190	
acc tac cac aca acc tcg tat ctc ctg att cac gac ggc gac cgc gct	624
Thr Tyr His Thr Ser Tyr Leu Leu Ile His Asp Gly Asp Arg Ala	
195 200 205	
gtt gta act tac gag ggc gat act agt gcg ggc tat aat cat gat gtc	672
Val Val Thr Tyr Glu Gly Asp Thr Ser Ala Gly Tyr Asn His Asp Val	
210 215 220	
tcc ata ctt cgt gcg tgg atc cgt act aca aaa ata gtt ggt gat cat	720



450	455	460	
atg	cg	tg	1440
Met	Arg	Trp	
465	470	475	480
ggt	tta	gtc	1488
Gly	Leu	Gly	
485	490	495	
gag	gtc	gac	1536
Glu	Val	Asp	
500	505	510	
gcc	gtc	cac	1584
Ala	Val	His	
515	520	525	
cca	caa	gat	1632
Pro	Gln	Asp	
530	535	540	
ctc	gtt	gca	1680
Leu	Val	Ala	
545	550	555	560
aag	acc	ttc	1728
Lys	Thr	Phe	
565	570	575	
ggc	cct	gag	1776
Gly	Pro	Glu	
580	585	590	
ggg	gcc	ggg	1824
Gly	Ala	Gly	
595	600	605	
cag	gtt	agg	1872
Gln	Val	Arg	
610	615	620	
ccc	ggt	gga	1920
Pro	Gly	Gly	
625	630	635	640
agt	gcc	ctt	1968
Ser	Ala	Leu	
645	650	655	
ggc	gga	tta	2016
Gly	Gly	Leu	
660	665	670	
ttc	tcc	cct	2064
Phe	Ser	Pro	
675	680	685	
ggg	cat	atc	
Gly	His	Ile	
	Trp	Trp	

ggg act ttg tat acc cga act tgg tca aca tct ggc ttt tct agt gat	2112
Gly Thr Leu Tyr Thr Arg Thr Trp Ser Thr Ser Gly Phe Ser Ser Asp	
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ttc tcc ccc cct gaa gcg gcc gct cct gct atg gct gct acc ccc ggg	2160
Phe Ser Pro Pro Glu Ala Ala Ala Pro Ala Met Ala Ala Thr Pro Gly	
705 710 715 720	
ctg ccc cat tct acc cca cct gtt agc gat att tgg gtg cta cca ccc	2208
Leu Pro His Ser Thr Pro Pro Val Ser Asp Ile Trp Val Leu Pro Pro	
725 730 735	
ccc tca gag gag ttt cag gtt gat gca gca cct gtg ccc cct gcc cct	2256
Pro Ser Glu Glu Phe Gln Val Asp Ala Ala Pro Val Pro Pro Ala Pro	
740 745 750	
gac cct gct gga ttg ccc ggt ccc gtt gtg ctt acc ccc ccc ccc cct	2304
Asp Pro Ala Gly Leu Pro Gly Pro Val Val Leu Thr Pro Pro Pro Pro	
755 760 765	
ccc cct gtg cat aag cca tca ata ccc ccg cct tcc cgt aac cgt cgt	2352
Pro Pro Val His Lys Pro Ser Ile Pro Pro Pro Ser Arg Asn Arg Arg	
770 775 780	
ctc ctc tat acc tat cct gac ggc gct aag gtg tat gca ggg tca ctg	2400
Leu Leu Tyr Thr Tyr Pro Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu	
785 790 795 800	
ttt gaa tca gac tgt gac tgg ctg gtt aat gcc tca aac ccg ggc cat	2448
Phe Glu Ser Asp Cys Asp Trp Leu Val Asn Ala Ser Asn Pro Gly His	
805 810 815	
cgt ccc gga ggt ggc ctc tgc cat gcc ttt tac caa cgt ttt cca gaa	2496
Arg Pro Gly Gly Leu Cys His Ala Phe Tyr Gln Arg Phe Pro Glu	
820 825 830	
gcg ttt tac cca act gaa ttc atc atg cgt gag ggt ctt gca gca tac	2544
Ala Phe Tyr Pro Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr	
835 840 845	
acc ttg acc ccg cgc cct atc att cat gca gtc gct ccc gat tat agg	2592
Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg	
850 855 860	
gtt gag cag aac ccg aag agg ctt gag gca gcg tac cgt gaa act tgt	2640
Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys	
865 870 875 880	
tcc cgt cgt ggc acc gct gcc tac ccg ctt ttg ggt tcg ggt ata tac	2688
Ser Arg Arg Gly Thr Ala Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr	
885 890 895	
cag gtc cct gtt agc ctc agt ttt gat gcc tgg gaa cgt aat cac cgc	2736
Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu Arg Asn His Arg	
900 905 910	

ccc ggc gat gag ctt tac ttg acc gag ccc gct gca aat tgg ttt gag	2784
Pro Gly Asp Glu Leu Tyr Leu Thr Glu Pro Ala Ala Asn Trp Phe Glu	
915 920 925	
gct aat aag ccg gcg cag ccg gtg ctc acc ata act gag gac acg gcc	2832
Ala Asn Lys Pro Ala Gln Pro Val Leu Thr Ile Thr Glu Asp Thr Ala	
930 935 940	
cgt acg gcc aac ctg gca ttg gag att gat gcc gct aca gag gtc ggc	2880
Arg Thr Ala Asn Leu Ala Leu Glu Ile Asp Ala Ala Thr Glu Val Gly	
945 950 955 960	
cgt gct tgt gcc ggt tgc acc atc agc cct ggc att gtg cac tat cag	2928
Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile Val His Tyr Gln	
965 970 975	
ttt acc gcc ggg gtc ccg ggc tcg ggc aag tca agg tcc ata caa cag	2976
Phe Thr Ala Gly Val Pro Gly Ser Gly Lys Ser Arg Ser Ile Gln Gln	
980 985 990	
gga gat gtc gat gtg gtt gtg ccc acc ccg gag ctt cgt aat agt	3024
Gly Asp Val Asp Val Val Val Pro Thr Arg Glu Leu Arg Asn Ser	
995 1000 1005	
tgg cgc cgc ccg ggt ttt gcg gcc ttc aca ccc cac aca gcg gcc cgt	3072
Trp Arg Arg Arg Gly Phe Ala Ala Phe Thr Pro His Thr Ala Ala Arg	
1010 1015 1020	
gtt act atc ggc cgc gtt gtg att gat gag gct cca tct ctc ccg	3120
Val Thr Ile Gly Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro	
1025 1030 1035 1040	
cca cac ctg ttg ctg tta cat atg cag ccg gcc tcc tcg gtc cat ctc	3168
Pro His Leu Leu Leu His Met Gln Arg Ala Ser Ser Val His Leu	
1045 1050 1055	
ctc ggt gac cca aat cag atc cct gct att gat ttt gag cac gcc ggc	3216
Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly	
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ctg gtc cct gcg atc cgt ccc gag ctt gcg cca acg agc tgg tgg crc	3264
Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa	
1075 1080 1085	
gtt aca cac cgt tgc ccg gat gtg tgc gag ctc ata cgc gga gcc	3312
Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala	
1090 1095 1100	
tac cct aaa atc cag acc acg agc cgt gtg cta cgg tcc ctg ttt tgg	3360
Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp	
1105 1110 1115 1120	
aat gaa ccg gcc att ggc cag aag ttg gtt ytc acg cag gcg gca aag	3408
Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys	
1125 1130 1135	
gct gct aac cct ggt gcg att acg gtc cac gaa gct cag ggt gcc acc	3456

Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr			
1140	1145	1150	
ttc aca gag acc aca atc ata gcc acg gcc gac ggc agg ggc ctt atc			3504
Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile			
1155	1160	1165	
cag tca tcc cgg gct cat gct ata gtt gca ctt act cgc cac act gag			3552
Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu			
1170	1175	1180	
aag tgt gtt atc ctg gat gcc ccc ggc ctg ctt cgt gag gtc ggc att			3600
Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile			
1185	1190	1195	1200
tcg gat gtg att gtc aac aac ttt ttc ctt gct ggt ggc gag gtc ggc			3648
Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly			
1205	1210	1215	
crc cac cgc cct tct gtg ata cct cgc ggt aac cct gat caa aac ctc			3696
Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu			
1220	1225	1230	
ggg act tta cag gcc ttc ccg ccg tcc tgt caa att agt gct tac cat			3744
Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His			
1235	1240	1245	
cag ttg gct gag gaa ctg ggc cat cgc ccg gcc cct gtc gcc gcc gtc			3792
Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val			
1250	1255	1260	
ttg ccc cct tgc cct gag ctt gag cag ggc ctg ctc tac atg cca cag			3840
Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln			
1265	1270	1275	1280
gag ctc act gtg tcc gat agt gtg ttg gtt ttt gag ctt acg gat ata			3888
Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile			
1285	1290	1295	
gtt cat tgc cgc atg gcc gct cca agc cag cga aag gct gtt ctc tca			3936
Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val Leu Ser			
1300	1305	1310	
aca ctt gtg ggg agg tat ggc cgt agg acg aaa cta tat gag gcg gcg			3984
Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala			
1315	1320	1325	
cat tca gat gtt cgt gag tcc cta gct agg ttc atc cct act atc ggg			4032
His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly			
1330	1335	1340	
cct gtt cag gct acc aca tgt gag ttg tat gag ttg gtt gag gct atg			4080
Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met			
1345	1350	1355	1360
gtg gag aaa ggt cag gac ggc tct gca gtc tta gag ctt gat ctt tgt			4128
Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu Leu Asp Leu Cys			

1365	1370	1375		
aat cgt gat gtc tcg cgc atc aca ttt ttc caa aaa gwc tgc aac aag Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys Xaa Cys Asn Lys 1380	1385	1390	4176	
ttt aca act ggt gag acc atc gcc cac ggc aag gtt ggc cag ggt ata Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val Gly Gln Gly Ile 1395	1400	1405	4224	
tcg gcc tgg agt aag acc ttc tgc gct ctg ttc ggc ccg tgg ttc cgc Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg 1410	1415	1420	4272	
gcc att gaa aaa gaa ata ttg gcc ctg ctc ccg cct aat atc ttt tat Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr 1425	1430	1435	1440	4320
ggc gac gct tat gag gag tca gtt ttt gcc gct gtg tcc ggg gcg Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Ala Val Ser Gly Ala 1445	1450	1455	4368	
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cag aat aat ttc tct ctt ggc ctt gag tgt gtg gtt atg gag gag tgc Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val Met Glu Glu Cys 1475	1480	1485	4464	
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cat tct ggt gag cct ggt acc ctt ctt tgg aat acc gtc tgg aat atg His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn Met 1525	1530	1535	4608	
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cgc aat gca gct gcc tta att gct ggc tgt ggg ctc aaa ttg aag gtt Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val 1570	1575	1580	4752	
gat tac cgc cct atc ggg ctg tat gct ggg gtg gtg gtg gcc ccc ggt Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly 1585	1590	1595	1600	4800

ttg ggg aca ctg ccc gat gtg gtg cgt ttt gct ggt cgg ttg tct gaa	4848
Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu	
1605 1610 1615	
aag aat tgg ggc ccc ggc ccg gaa cgt gct gag cag ctg cgt ctt gct	4896
Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala	
1620 1625 1630	
gtc tgc gac ttc ctt cga ggg ttg acg aat gtt gct cag gtc tgt gtt	4944
Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val	
1635 1640 1645	
gat gtt gtg tcc cgt gtc tat gga gtc agc ccc ggg ctc gta cat aac	4992
Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn	
1650 1655 1660	
ctt att ggc atg ctg cag acc atc gcc gat ggc aag gcc cac ttt aca	5040
Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr	
1665 1670 1675 1680	
gag act att aaa cct gta ctt gat ctc aca aat tcc atc ata cag cgg	5088
Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg	
1685 1690 1695	
gtg gaa tgaataacat gtctttgca tcgccccatgg gatcacc atg cgc cct agg	5143
Val Glu	Met Arg Pro Arg
	1700
gct gtt ctg ttg ttc ctc atg ttt ctg cct atg ctg ccc gcg cca	5191
Ala Val Leu Leu Phe Leu Met Phe Leu Pro Met Leu Pro Ala Pro	
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ccg gcc ggt cag ccg tct ggc cgt cgc cgt ggg cgg cgc agc ggc ggt	5239
Pro Ala Gly Gln Pro Ser Gly Arg Arg Gly Arg Arg Ser Gly Gly	
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gcc ggc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc	5287
Ala Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala	
1735 1740 1745 1750	
ctc ccc tat att cat cca acc aac ccc ttc gcc gat gtc gtt tca	5335
Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser	
1755 1760 1765	
caa ccc ggg gct gga act cgc cct cga cag ccg ccc cgc ccc ctc ggt	5383
Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly	
1770 1775 1780	
tcc gct tgg cgt gac cag tcc aag cgc ccc tcc gtt gcc ccc cgt cgt	5431
Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val Ala Pro Arg Arg	
1785 1790 1795	
cga tct acc cca gct ggg gct gcg ccc tca act gcc ata tca cca gcc	5479
Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Ile Ser Pro Ala	
1800 1805 1810	

cct gat aca gct cct gta cct gat gtt gac tca cgt ggt gct att ttg Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu 1815 1820 1825 1830	5527
cgc cgg cag tac aat ttg tct acg tcc ccg ctt aca tca tct gtt gct Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Ser Val Ala 1835 1840 1845	5575
tct ggt act aat ctg gtt ctc tat gct gcc ccg ctg aac cct ctc ttg Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Asn Pro Leu Leu 1850 1855 1860	5623
cct ctt cag gat ggc acc aac act cat att atg gct act gag gca tct Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser 1865 1870 1875	5671
aat tac gcc cag tat cgg gtt cgg gct acg att cgt tat cgc ccg Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile Arg Tyr Arg Pro 1880 1885 1890	5719
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cct caa act aca act acc cct act tct gtt gac atg aat tct atc act Pro Gln Thr Thr Pro Thr Ser Val Asp Met Asn Ser Ile Thr 1915 1920 1925	5815
tct act gat gtc agg atc ttg gtc cag ccc ggt ata gcc tcc gag tta Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile Ala Ser Glu Leu 1930 1935 1940	5863
gtc atc cct agt gaa cgc ctt cac tac cgc aac caa ggc tgg cgc tct Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln Gly Trp Arg Ser 1945 1950 1955	5911
gtt gag acc acg ggt gtg gcc gaa gag gag gct acc tcc ggt ctg gta Val Glu Thr Thr Gly Val Ala Glu Glu Glu Ala Thr Ser Gly Leu Val 1960 1965 1970	5959
atg ctt tgt att cat ggc tcc cct gtt aac tcc tac act aat aca cct Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr Thr Asn Thr Pro 1975 1980 1985 1990	6007
tac acc ggt gca ttg ggg ctt ctt gat ttt gca tta gaa ctt gaa ttt Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu Glu Leu Glu Phe 1995 2000 2005	6055
aga aat ttg aca ccc ggg aac act aac acc cgt gtt tcc cgg tat act Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val Ser Arg Tyr Thr 2010 2015 2020	6103
agc aca gcc cgc cac cgg ctg cgc cgc ggt gct gat ggg acc gct gag Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu 2025 2030 2035	6151
ctc acc acc aca gca gcc aca cgc ttc atg aag gat ttg cat ttt act	6199

Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr	2040	2045	2050	
ggt acg aac ggc gtt ggt gag gtg ggt cgt ggt att gcc ctg act ctg				6247
Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu				
2055	2060	2065	2070	
ttt aat ctt gct gat acg ctt ctt ggt ggt tta ccg aca gaa ttg att				6295
Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile				
2075	2080	2085		
tcg tcg gct ggg ggt caa ctg ttt tac tcc cgc cct gtt gtc tcg gcc				6343
Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala				
2090	2095	2100		
aat ggc gag cca aca gta aag tta tac aca tct gtt gag aat gcg cag				6391
Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln				
2105	2110	2115		
caa gac aag ggc atc acc att cca cac gac ata gat tta ggt gac tcc				6439
Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu Gly Asp Ser				
2120	2125	2130		
cgt gtg gtt atc cag gat tat gat aac cag cac gaa caa gat cga cct				6487
Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro				
2135	2140	2145	2150	
acc ccg tca cct gcc ccc tcc cgc cct ttc tca gtt ctt cgt gcc aat				6535
Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn				
2155	2160	2165		
gat gtt ttg tgg ctc tct ctc act gcc gct gag tac grc cag acc acg				6583
Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Xaa Gln Thr Thr				
2170	2175	2180		
tat ggg tcg tcc acc aac cct atg tat gtc tct gat aca gtc acg ctt				6631
Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Leu				
2185	2190	2195		
gtt aat gta gcc act ggt gct cag gct gtt gcc cgc tct ctt gac tgg				6679
Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser Leu Asp Trp				
2200	2205	2210		
tct aaa gtt act ctg gat ggt cgc cct ctt act acc att cag cag tat				6727
Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr				
2215	2220	2225	2230	
tct aag aaa ttt tat gtt ctc ccg ctt cgs ggg aag ctg tcc ttt tgg				6775
Ser Lys Lys Phe Tyr Val Leu Pro Leu Xaa Gly Lys Leu Ser Phe Trp				
2235	2240	2245		
gag gct ggt acg acc aag gcc ggc tac ccg tat aat tat aat acc act				6823
Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr				
2250	2255	2260		
gct agt gac caa att ttg att gag aac gcg gcc ggt cac cgt gtc gcc				6871
Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Gly His Arg Val Ala				

2265	2270	2275	
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2280	2285	2290	
gcg gtc ggt gta cta gct cca cat tcg gcc ctt gct gtt ctc gag gat Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val Leu Glu Asp			6967
2295	2300	2305	2310
act gtt gat tat cct gct cgt gcc cat act ttt gat gat ttc tgc ccg Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro			7015
2315	2320	2325	
gag tgt cgc acc ctt ggt ctg cag ggt tgt gca ttc caa tct act att Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile			7063
2330	2335	2340	
gct gaa ctt cag cgt ctt aaa atg aag gta ggt aaa acc cgg gag tct Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser			7111
2345	2350	2355	
taattaattc cttttgtgcc cccttcgcag ttctttgg ctttatttct catttctgct ttccgcgctc cctggaaaaa aaaaaaaaaa a			7171 7202
<p>&lt;210&gt; 91  &lt;211&gt; 1698  &lt;212&gt; PRT  &lt;213&gt; Hepatitis E Virus</p> <p>&lt;220&gt;  &lt;223&gt; Xaa = Unknown or Other at position 174</p> <p>&lt;223&gt; Xaa = Unknown or Other at position 363</p> <p>&lt;223&gt; Xaa = Unknown or Other at position 1088</p> <p>&lt;223&gt; Xaa = Unknown or Other at position 1131</p> <p>&lt;223&gt; Xaa = Unknown or Other at position 1217</p> <p>&lt;223&gt; Xaa = Unknown or Other at position 1389</p> <p>&lt;400&gt; 91</p>			
Pro Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Ala Ala Asn			
1	5	10	15
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val			
20	25	30	
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe			
35	40	45	
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn			
50	55	60	
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val			
65	70	75	80
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg			
85	90	95	
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala			

100	105	110
Pro	Thr	Arg
Gly	Pro	Ala
115	120	125
Leu	Pro	Ala
Asp	Arg	Thr
Tyr	Cys	Phe
130	135	140
Ala	Phe	Ala
Ala	Glu	Thr
Gly	Val	Ala
145	150	155
Trp	Pro	Ala
Asp	Val	Glu
Ala	Met	Ala
Arg	His	Gly
165	170	175
Leu	Tyr	Ala
Ala	Leu	His
Leu	Pro	Pro
Glu	Val	Leu
180	185	190
Thr	Tyr	His
Thr	Thr	Ser
Tyr	Leu	Leu
Ile	His	Asp
Gly	Asp	Arg
195	200	205
Val	Val	Thr
Tyr	Glu	Gly
Asp	Thr	Ser
Ala	Gly	Tyr
195	215	220
Ser	Ile	Leu
Leu	Arg	Ala
Trp	Ile	Arg
Thr	Thr	Lys
Ile	Val	Gly
225	230	235
Pro	Leu	Val
Ile	Glu	Arg
Val	Arg	Ala
Ile	Gly	Cys
245	250	255
Leu	Leu	Thr
Ala	Ala	Pro
Glu	Pro	Ser
260	265	270
Pro	Arg	Ser
Thr	Glu	Val
Tyr	Val	Arg
Ser	Ile	Phe
Gly	Pro	Gly
275	280	285
Ser	Pro	Ser
Leu	Phe	Pro
Ser	Ala	Cys
290	295	300
Ala	Val	Pro
Val	His	Ile
Trp	Asp	Arg
Leu	Met	Leu
Phe	Gly	Gly
305	310	315
Leu	Asp	Asp
Gln	Ala	Phe
Cys	Cys	Ser
325	330	335
Gly	Ile	Ser
Tyr	Lys	Val
340	345	350
Trp	Asn	Ala
Ser	Glu	Asp
Ala	Leu	Thr
Xaa	Ile	Thr
Ile	Ala	Tyr
355	360	365
Leu	Thr	Ile
Cys	His	Gln
Arg	Tyr	Leu
370	375	380
Gly	Met	Arg
Arg	Leu	Gly
385	390	395
Leu	Tyr	Ser
Trp	Leu	Phe
Glu	Lys	Ser
Gly	Arg	Asp
405	410	415
Arg	Gln	Leu
Gln	Phe	Tyr
Ala	Gln	Cys
420	425	430
Phe	His	Leu
Asp	Pro	Arg
435	440	445
Arg	Cys	Arg
Thr	Phe	Leu
Lys	Lys	Val
450	455	460
Met	Arg	Trp
Trp	Leu	Gly
Gln	Glu	Cys
465	470	475
Gly	Leu	Val
Gly	Asp	His
His	Gly	Asp
485	490	495
Glu	Val	Asp
Asp	Pro	Ala
Glu	Pro	Ala
500	505	510
Ala	Val	His
Gly	His	Gln
515	520	525
Pro	Gln	Asp
Ile	Ala	Ala
Arg	Ala	Ser
530	535	540
Leu	Val	Ala
Ala	Ser	Pro
Asp	Arg	Leu
Glu	Cys	Arg
545	550	555
Leu	Val	Leu
Gly	Asn	
		560

Lys Thr Phe Arg Thr Thr Val Val Asp Gly Ala His Leu Glu Ala Asn  
 565 570 575  
 Gly Pro Glu Gln Tyr Val Leu Ser Phe Asp Ala Ser Arg Gln Ser Met  
 580 585 590  
 Gly Ala Gly Ser His Ser Leu Thr Tyr Glu Leu Thr Pro Ala Gly Leu  
 595 600 605  
 Gln Val Arg Ile Ser Ser Asn Gly Leu Asp Cys Thr Ala Thr Phe Pro  
 610 615 620  
 Pro Gly Gly Ala Pro Ser Ala Ala Pro Gly Glu Val Ala Ala Phe Cys  
 625 630 635 640  
 Ser Ala Leu Tyr Arg Tyr Asn Arg Phe Thr Gln Arg His Ser Leu Thr  
 645 650 655  
 Gly Gly Leu Trp Leu His Pro Glu Gly Leu Leu Gly Ile Phe Pro Pro  
 660 665 670  
 Phe Ser Pro Gly His Ile Trp Glu Ser Ala Asn Pro Phe Cys Gly Glu  
 675 680 685  
 Gly Thr Leu Tyr Thr Arg Thr Trp Ser Thr Ser Gly Phe Ser Ser Asp  
 690 695 700  
 Phe Ser Pro Pro Glu Ala Ala Ala Pro Ala Met Ala Ala Thr Pro Gly  
 705 710 715 720  
 Leu Pro His Ser Thr Pro Pro Val Ser Asp Ile Trp Val Leu Pro Pro  
 725 730 735  
 Pro Ser Glu Glu Phe Gln Val Asp Ala Ala Pro Val Pro Pro Ala Pro  
 740 745 750  
 Asp Pro Ala Gly Leu Pro Gly Pro Val Val Leu Thr Pro Pro Pro Pro  
 755 760 765  
 Pro Pro Val His Lys Pro Ser Ile Pro Pro Pro Ser Arg Asn Arg Arg  
 770 775 780  
 Leu Leu Tyr Thr Tyr Pro Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu  
 785 790 795 800  
 Phe Glu Ser Asp Cys Asp Trp Leu Val Asn Ala Ser Asn Pro Gly His  
 805 810 815  
 Arg Pro Gly Gly Leu Cys His Ala Phe Tyr Gln Arg Phe Pro Glu  
 820 825 830  
 Ala Phe Tyr Pro Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr  
 835 840 845  
 Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg  
 850 855 860  
 Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys  
 865 870 875 880  
 Ser Arg Arg Gly Thr Ala Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr  
 885 890 895  
 Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu Arg Asn His Arg  
 900 905 910  
 Pro Gly Asp Glu Leu Tyr Leu Thr Glu Pro Ala Ala Asn Trp Phe Glu  
 915 920 925  
 Ala Asn Lys Pro Ala Gln Pro Val Leu Thr Ile Thr Glu Asp Thr Ala  
 930 935 940  
 Arg Thr Ala Asn Leu Ala Leu Glu Ile Asp Ala Ala Thr Glu Val Gly  
 945 950 955 960  
 Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile Val His Tyr Gln  
 965 970 975  
 Phe Thr Ala Gly Val Pro Gly Ser Gly Lys Ser Arg Ser Ile Gln Gln  
 980 985 990  
 Gly Asp Val Asp Val Val Val Pro Thr Arg Glu Leu Arg Asn Ser  
 995 1000 1005  
 Trp Arg Arg Arg Gly Phe Ala Ala Phe Thr Pro His Thr Ala Ala Arg

1010	1015	1020
Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro		
1025	1030	1035
Pro His Leu Leu Leu His Met Gln Arg Ala Ser Ser Val His Leu		
1045	1050	1055
Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly		
1060	1065	1070
Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa		
1075	1080	1085
Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala		
1090	1095	1100
Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp		
1105	1110	1115
Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys		
1125	1130	1135
Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr		
1140	1145	1150
Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile		
1155	1160	1165
Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu		
1170	1175	1180
Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile		
1185	1190	1195
Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly		
1205	1210	1215
Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu		
1220	1225	1230
Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His		
1235	1240	1245
Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val		
1250	1255	1260
Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln		
1265	1270	1275
Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile		
1285	1290	1295
Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val Leu Ser		
1300	1305	1310
Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala		
1315	1320	1325
His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly		
1330	1335	1340
Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met		
1345	1350	1355
Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu Leu Asp Leu Cys		
1365	1370	1375
Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys Xaa Cys Asn Lys		
1380	1385	1390
Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val Gly Gln Gly Ile		
1395	1400	1405
Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg		
1410	1415	1420
Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr		
1425	1430	1435
Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Ala Val Ser Gly Ala		
1445	1450	1455
Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr		
1460	1465	1470

Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val Met Glu Glu Cys  
                  1475                 1480                 1485  
 Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Val Arg Ser Ala  
                  1490                 1495                 1500  
 Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys  
                  1505                 1510                 1515                 1520  
 His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn Met  
                  1525                 1530                 1535  
 Ala Ile Ile Ala His Cys Tyr Glu Phe Arg Asp Phe Arg Val Ala Ala  
                  1540                 1545                 1550  
 Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp Tyr Arg Gln Ser  
                  1555                 1560                 1565  
 Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val  
                  1570                 1575                 1580  
 Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly  
                  1585                 1590                 1595                 1600  
 Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu  
                  1605                 1610                 1615  
 Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala  
                  1620                 1625                 1630  
 Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val  
                  1635                 1640                 1645  
 Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn  
                  1650                 1655                 1660  
 Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr  
                  1665                 1670                 1675                 1680  
 Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg  
                  1685                 1690                 1695  
 Val Glu

<210> 92  
 <211> 660  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 481  
 <223> Xaa = Unknown or Other at position 542  
 <223> Xaa = Unknown or Other at position 595

<400> 92  
 Met Arg Pro Arg Ala Val Leu Leu Phe Leu Met Phe Leu Pro Met  
                  1                 5                 10                 15  
 Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg  
                  20                 25                 30  
 Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser  
                  35                 40                 45  
 Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala  
                  50                 55                 60  
 Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro  
                  65                 70                 75                 80  
 Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val  
                  85                 90                 95  
 Ala Pro Arg Arg Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala

100	105	110	
Ile Ser Pro Ala Pro Asp Thr Ala	Pro Val Pro Asp Val Asp Ser Arg		
115	120	125	
Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr			
130	135	140	
Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu			
145	150	155	160
Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala			
165	170	175	
Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile			
180	185	190	
Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser			
195	200	205	
Ile Ser Phe Trp Pro Gln Thr Thr Thr Pro Thr Ser Val Asp Met			
210	215	220	
Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile			
225	230	235	240
Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln			
245	250	255	
Gly Trp Arg Ser Val Glu Thr Thr Gly Val Ala Glu Glu Glu Ala Thr			
260	265	270	
Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr			
275	280	285	
Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu			
290	295	300	
Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val			
305	310	315	320
Ser Arg Tyr Thr Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp			
325	330	335	
Gly Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe Met Lys Asp			
340	345	350	
Leu His Phe Thr Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile			
355	360	365	
Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro			
370	375	380	
Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro			
385	390	395	400
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val			
405	410	415	
Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp			
420	425	430	
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu			
435	440	445	
Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val			
450	455	460	
Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr			
465	470	475	480
Xaa Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp			
485	490	495	
Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg			
500	505	510	
Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr			
515	520	525	
Ile Gln Gln Tyr Ser Lys Lys Phe Tyr Val Leu Pro Leu Xaa Gly Lys			
530	535	540	
Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn			
545	550	555	560

Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly  
                   565                  570                  575  
 His Arg Val Ala Ile Ser Thr Tyr Thr Ser Leu Gly Ala Gly Pro  
                   580                  585                  590  
 Thr Ser Xaa Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala  
                   595                  600                  605  
 Val Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp  
                   610                  615                  620  
 Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe  
                   625                  630                  635                  640  
 Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys  
                   645                  650                  655  
 Thr Arg Glu Ser  
                   660

<210> 93  
 <211> 122  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> ORF3 HEV US-1

<400> 93  
 Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys Ala Leu  
   1                  5                  10                  15  
 Gly Leu Phe Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg  
   20                  25                  30  
 His Arg Pro Val Ser Arg Leu Ala Val Ala Val Gly Gly Ala Ala Ala  
   35                  40                  45  
 Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser  
   50                  55                  60  
 Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser Phe  
   65                  70                  75                  80  
 His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser  
   85                  90                  95  
 Val Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro Pro Val  
   100                  105                  110  
 Val Asp Leu Pro Gln Leu Gly Leu Arg Arg  
   115                  120

<210> 94  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer US5P3S/20

<400> 94

tggcattact actgccatttg

20

<210> 95  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer US5P45S/20

<400> 95  
 caattctgcc ttggcgaatg 20

<210> 96  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer US5P296A

<400> 96  
 agggaaacacc gatgcagaac 20

<210> 97  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer US5P243A/20

<400> 97  
 tccaaacctcc aagcaacgac 20

<210> 98  
 <211> 199  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Clone: 199con

<400> 98  
 caattctgcc ttggcgaatg ctgtggtggt tcggccgtt ctttctcgta tgcaaactga 60  
 gattcttatt aatttgc aacccggca gttggtcttc cgcctgagg tgctttggaa 120  
 tcattcctatc cagcgggtta tacataatga attagagcag tactgccggg cccgggctgg 180  
 tcgttgcttg gaggttggaa 199

<210> 99  
 <211> 25  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> JE orf1-s

<400> 99  
 gttctgcattc ggtgtttcct tagac 25

<210> 100  
 <211> 26  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> JE orf1-a  
  
 <400> 100  
 gaatcaggag atacgagggtt gtgtgg 26

<210> 101  
 <211> 331  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> us2-320

<400> 101  
 gttctgcac ggtgtttccct tagaccggtc ggccgagatg ttcaagcgctg gtattctgcc 60  
 cctaccggcgtg gtcctgcggc caattggccgc cgctccggcgt tgctgtggctc ccccccgtgc 120  
 gaccggcacct attgttttga tggattttcc cggtgtgttctt ttgtgcaga gaccgggtgtg 180  
 gccccttact ctttgcatga cctttggcca gctgatgttgc cagaggctat ggcccgccat 240  
 gggatgacac gcttatacgc cgcaactgcac cttccccccg aggtgctgtc accaccggc 300  
 accataccaca caacctcgta tctcctgatt c 331

<210> 102  
 <211> 1186  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> us2-1168

<400> 102  
 ctcactgtgt ccgatagtggt gttggttttt gagcttacgg atatagtcca ctggcgatag 60  
 gccggcccaa gccagcgaaa ggctgttctc tcaacgccttgc tggggaggtt cggccgttagg 120  
 actaaattat atgaggcgcc gcattcagat gtccgtgagt cccttagcgag gtttatcccc 180  
 accatcgggc ctgttcgggc taccacatgt gagctgtacg agctggttga agccatggta 240  
 gagaagggtc aggacggatc tgccgtccta gagctcgacc tttgcaatcg tgacgtctcg 300  
 cgcatcacat ttttccaaaa ggattgcaat aagtttacaa ctgtgtgagac tatcgcccat 360  
 ggcaagggtt gccaggccat atcggcctgg agcaagaccc tctgtgtctc gtttggcccg 420  
 tggttcccgcc ccattgaaaa ggaaatattt gcccctactcc cgccctaataat cttttatggc 480  
 gacgcctatg aggagtcaatg gtttgcgtcc gctgtgtccg gggcagggtc atgtatggta 540  
 tttgaaaatg acttctcaga gtttgcacatg acccagaata atttctctc cggccttgag 600  
 tgggtgttta tgaggaggatg cggcatgccc caatggttaa ttaggttgc ccatctggc 660  
 cggtcagccct ggattttgc ggcggccgaag gagtctcttta aggggttttgaagaagac 720  
 tctggtgagc ctggtaaccct tctctggaaac actgtctggaa acatggcgat tatagcacat 780  
 tgctayagat tccgtgactt tcgtgttgcc gccttcaagg gtgtatgattc agtggctc 840  
 tggtagtgact accgacagrrg cctgttaacgcg gctgccttaa ttgcaggctg tgggctcaaa 900  
 ttgaagggtt attaccggccc tatcggttca tatgtctggag tgggtgtggc ccccggtttg 960  
 gggacactgc ccgatgtgttgc gctgtttgc ggtcggttat ctgagaagaa ttggggccct 1020  
 ggcccgagc gtgctgagca gctgcgtctt gctgtttgtt attccttcg agggttgc 1080  
 aatgttgcgc agtctgtgt tgatgttgc tcccggtct atggaggttag ccccggtctg 1140  
 gtacataacc ttattggcat gctgcagacc atcgccgatg gcaagg 1186

<210> 103  
 <211> 23  
 <212> DNA  
 <213> Hepatitis E Virus

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<220>
<223> JE hevdf2/3 s1

<400> 103
gttcccgcttg gcgtgaccag tcc 23

<210> 104
<211> 23
<212> DNA
<213> Hepatitis E virus

<220>
<223> JE hevdf2/3 a1

<400> 104
gagtcAACAT caggtacagg agc 23

<210> 105
<211> 130
<212> DNA
<213> Hepatitis E Virus

<220>
<223> us2-135

<400> 105
gttcccgcttg gcgtgaccag tcccagcgcc cctccgctgc ccccccgtcg tcatctgccc 60
cagctggggc tgccgcgtg actgcccgtg caccggctcc tgacacagct cctgtacctg 120
atgttgcactc 130

<210> 106
<211> 26
<212> DNA
<213> Hepatitis E Virus

<220>
<223> JE hevdf1-s1

<400> 106
gatgtcattt tgtgttgctg ctcacc 26

<210> 107
<211> 23
<212> DNA
<213> Hepatitis E Virus

<220>
<223> hev216 a1

<400> 107
cgtcctacag cgccatggta ctg 23

<210> 108
<211> 564
<212> DNA
<213> Hepatitis E Virus

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<220>  
 <223> us2-563

<400> 108

tcaccatgc	cttatgttcc	ttaccctcg	tcaacggagg	tgtatgtccg	gtcttatattt	60
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gctgtcccg	ttcacatctg	ggatcrgctc	atgcttttgc	gtgccaccct	gracgatcag	180
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Asn Glu Gly Trp Asn Ala Ser Glu Asp Ala Leu Thr Ala Val Ile Thr			

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gcg gcc tat ctg acc atc tgc cat cag cgt tac ctt cgc acc cag gcg Ala Ala Tyr Leu Thr Ile Cys His Gln Arg Tyr Leu Arg Thr Gln Ala			1205
375	380	385	390
att tcc aag ggc atg cgc cgg ttg gag gtt gag cat gct cag aaa ttt Ile Ser Lys Gly Met Arg Arg Leu Glu Val Glu His Ala Gln Lys Phe			1253
395	400	405	
atc aca aga ctc tac agc tgg cta ttt gag aag tct ggc cgt gac tac Ile Thr Arg Leu Tyr Ser Trp Leu Phe Glu Lys Ser Gly Arg Asp Tyr			1301
410	415	420	
atc ccc ggc cgc cag ctt caa ttt tat gca caa tgc cga cgg tgg ctt Ile Pro Gly Arg Gln Leu Gln Phe Tyr Ala Gln Cys Arg Arg Trp Leu			1349
425	430	435	
tct gca ggc ttc cac cta rac ccc agg rtg ctt gtc ttt gat gaa tca Ser Ala Gly Phe His Leu Xaa Pro Arg Xaa Leu Val Phe Asp Glu Ser			1397
440	445	450	
gtg cca tgc cgt tgc agg acg ttt ttg aag aag gtc gcg ggt aaa ttc Val Pro Cys Arg Cys Arg Thr Phe Leu Lys Lys Val Ala Gly Lys Phe			1445
455	460	465	470
tgc tgt ttt atg cgg tgg ctg ggg cag gag tgt acc tgc ttc ttg gag Cys Cys Phe Met Arg Trp Leu Gly Gln Glu Cys Thr Cys Phe Leu Glu			1493
475	480	485	
cca gcc gag ggt tta gtt ggt gat caa ggt cat gac aac gag gcc tat Pro Ala Glu Gly Leu Val Gly Asp Gln Gly His Asp Asn Glu Ala Tyr			1541
490	495	500	
gaa ggt tct gag gtc gac cca gct gag cct gca cat ctt gat gtc tcg Glu Gly Ser Glu Val Asp Pro Ala Glu Pro Ala His Leu Asp Val Ser			1589
505	510	515	
ggg act tat gcc gtc cat ggg cac cag ctt gag gcc ctc tat agg gca Gly Thr Tyr Ala Val His Gly His Gln Leu Glu Ala Leu Tyr Arg Ala			1637
520	525	530	
ctt aat gtc cca cat gat att gcc gct cga gcc tcc cga cta acg gct Leu Asn Val Pro His Asp Ile Ala Ala Arg Ala Ser Arg Leu Thr Ala			1685
535	540	545	550
act gtt gag ctc gtt gct agt ccg gac cgc tta gag tgc cgc act gta Thr Val Glu Leu Val Ala Ser Pro Asp Arg Leu Glu Cys Arg Thr Val			1733
555	560	565	
ctt ggt aat aag acc ttc cgg acg acg gtg gtt gat ggc gcc cat ctt Leu Gly Asn Lys Thr Phe Arg Thr Thr Val Val Asp Gly Ala His Leu			1781
570	575	580	
gaa gcg aat ggc cct gag gag tat gtt ctg tca ttt gac gcc tct cgc Glu Ala Asn Gly Pro Glu Glu Tyr Val Leu Ser Phe Asp Ala Ser Arg			1829
585	590	595	

cag tct atg ggg gcc ggg tcg cac agc ctc act tat gag ctc acc cct	1877
Gln Ser Met Gly Ala Gly Ser His Ser Leu Thr Tyr Glu Leu Thr Pro	
600 605 610	
gcc ggt ctg cag gta aag att tca tct aat ggt ctg gat tgc act gcc	1925
Ala Gly Leu Gln Val Lys Ile Ser Ser Asn Gly Leu Asp Cys Thr Ala	
615 620 625 630	
aca ttc ccc ccy ggt ggc gcc cct agc gcc gcg ccg ggg gag gtg gcs	1973
Thr Phe Pro Xaa Gly Gly Ala Pro Ser Ala Ala Pro Gly Glu Val Xaa	
635 640 645	
gcc ttc tgc agt gct ctt tat aga tac aat agg ttc acc cag cgg cat	2021
Ala Phe Cys Ser Ala Leu Tyr Arg Tyr Asn Arg Phe Thr Gln Arg His	
650 655 660	
tcg ctg aca ggc gga cta tgg cta cat cct gag ggg ctg ctg ggt atc	2069
Ser Leu Thr Gly Gly Leu Trp Leu His Pro Glu Gly Leu Leu Gly Ile	
665 670 675	
ttc ccc cca ttc tcc cct ggg cat att tgg gag tct gct aac ccc ttt	2117
Phe Pro Pro Phe Ser Pro Gly His Ile Trp Glu Ser Ala Asn Pro Phe	
680 685 690	
tgc ggt gag ggg act ttg tat acc cga acc tgg tca acc tct ggt ttt	2165
Cys Gly Glu Gly Thr Leu Tyr Thr Arg Thr Trp Ser Thr Ser Gly Phe	
695 700 705 710	
tct agt gat ttc tcc ccc cct gag gcg gcc gct cct gct tcg gct gcc	2213
Ser Ser Asp Phe Ser Pro Pro Glu Ala Ala Ala Pro Ala Ser Ala Ala	
715 720 725	
gcc ccg ggg ttg ccc tac cct act cca cct gtt agt gat atc tgg gtg	2261
Ala Pro Gly Leu Pro Tyr Pro Thr Pro Pro Val Ser Asp Ile Trp Val	
730 735 740	
tta cca ccg ccc tca gag gaa tct cat gtt gat gct gca tct gta ccc	2309
Leu Pro Pro Ser Glu Glu Ser His Val Asp Ala Ala Ser Val Pro	
745 750 755	
tct gtt cct gag cct gct gga ttg acc agc cct att gtg ctt acc ccc	2357
Ser Val Pro Glu Pro Ala Gly Leu Thr Ser Pro Ile Val Leu Thr Pro	
760 765 770	
ccc ccc ccc cct ccc gtg cgt aag ccg gca aca tcc ccg cct ccc	2405
Pro Pro Pro Pro Pro Val Arg Lys Pro Ala Thr Ser Pro Pro Pro	
775 780 785 790	
cgc act cgc cgt ctc ctt tac acc tac ccc gac ggc gcc aag gtg tat	2453
Arg Thr Arg Arg Leu Leu Tyr Thr Tyr Pro Asp Gly Ala Lys Val Tyr	
795 800 805	
gcg ggg tca ttg tkt gag tca gac tgt gat tgg tta gtc aat gcc tca	2501
Ala Gly Ser Leu Xaa Glu Ser Asp Cys Asp Trp Leu Val Asn Ala Ser	
810 815 820	

aac cct ggc cat cgc ccc ggg ggt ggc ctc tgc cat gct ttt tat caa Asn Pro Gly His Arg Pro Gly Gly Leu Cys His Ala Phe Tyr Gln 825 830 835	2549
cgt ttc cca gaa gcg ttc tac tcg act gaa ttc atc atg cgc gag ggc Arg Phe Pro Glu Ala Phe Tyr Ser Thr Glu Phe Ile Met Arg Glu Gly 840 845 850	2597
ctt gca gca tac act tta acc ccg cgc cct att atc cat gca gtg gct Leu Ala Ala Tyr Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala 855 860 865 870	2645
ccc gac tat agg gtt gag caa aac ccg aag agg ctt gag gca gcg tac Pro Asp Tyr Arg Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr 875 880 885	2693
cgg gaa act tgc tcc cgt cgt ggc acc gct gcc tac ccg ctt ttg ggc Arg Glu Thr Cys Ser Arg Arg Gly Thr Ala Ala Tyr Pro Leu Leu Gly 890 895 900	2741
tcg ggt ata tac cag gtc cct gtt agc ctc agt ttt gat gcc tgg gaa Ser Gly Ile Tyr Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu 905 910 915	2789
cgc aat cac cgc ccc ggc gat gag ctt tac ttg aca gag ccc gcc gca Arg Asn His Arg Pro Gly Asp Glu Leu Tyr Leu Thr Glu Pro Ala Ala 920 925 930	2837
gcc tgg ttt gag gct aat aag ccg gcg cag ccg gcg ctt act ata act Ala Trp Phe Glu Ala Asn Lys Pro Ala Gln Pro Ala Leu Thr Ile Thr 935 940 945 950	2885
gag gac acg gcc cgt acg gcc aac ctg gca tta gag att gat gcc gcc Glu Asp Thr Ala Arg Thr Ala Asn Leu Ala Leu Glu Ile Asp Ala Ala 955 960 965	2933
aca gag gtt ggc cgt gct tgt gcc ggc tgc acc atc agc ccc ggg att Thr Glu Val Gly Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile 970 975 980	2981
gtg cac tat cag ttt acc gcc ggg gtc ccg ggc tca ggc aag tca agg Val His Tyr Gln Phe Thr Ala Gly Val Pro Gly Ser Gly Lys Ser Arg 985 990 995	3029
tcc ata caa cag gga gat gtc gat gtg gtg gtt gtg ccc acc cgg gag Ser Ile Gln Gln Gly Asp Val Asp Val Val Val Pro Thr Arg Glu 1000 1005 1010	3077
ctc cgt aac agc tgg cgt cgc cgg ggt ttt gcg gcc ttc aca cct cac Leu Arg Asn Ser Trp Arg Arg Gly Phe Ala Ala Phe Thr Pro His 1015 1020 1025 1030	3125
aca gcg gcc cgt gtt act atc ggc cgc cgc gtt gtg att gat gag gct Thr Ala Ala Arg Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala 1035 1040 1045	3173
cca tct ctc cca ccg cac ctg ctg tta cac atg cag cgg gcc tcc	3221

Pro Ser Leu Pro Pro His Leu Leu Leu His Met Gln Arg Ala Ser			
1050	1055	1060	
tcg gtc cat ctc ctt ggt gat cca aac cag att cct gct att gat ttt			3269
Ser Val His Leu Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe			
1065	1070	1075	
gag cat gcc ggc ctg gtc ccc gcg atc cgc ccc gag ctt gcg cca acg			3317
Glu His Ala Gly Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr			
1080	1085	1090	
agc tgg tgg cac gtt aca cac cgt tgc ccg gcc gat gtg tgc gag ctc			3365
Ser Trp Trp His Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu			
1095	1100	1105	1110
ata cgt ggg gcc tac ccc aaa att cag acc acg agc cgt gtg cta cg			3413
Ile Arg Gly Ala Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg			
1115	1120	1125	
tcc ctg ttt tgg aac gaa ccg gcc atc ggc caa aag ttg gtt ttt acg			3461
Ser Leu Phe Trp Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Phe Thr			
1130	1135	1140	
cag gct gct aag gct gcc aac cct ggt gcg att acg gtt cac gaa gct			3509
Gln Ala Ala Lys Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala			
1145	1150	1155	
cag ggt gct act ttc acg gag acc aca att ata gcc acg gcc gac gct			3557
Gln Gly Ala Thr Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala			
1160	1165	1170	
agg ggc ctc att cag tca tcc cgg gcc cat gct ata gtc gca ctc acc			3605
Arg Gly Leu Ile Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr			
1175	1180	1185	1190
cgc cat act gag aag tgt gtt att ttg gat gcc ccc ggc ttg ttg cgc			3653
Arg His Thr Glu Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg			
1195	1200	1205	
gag gtc ggc att tcg gat gtt att gtc aat aac ttt ttc ctt gcc ggt			3701
Glu Val Gly Ile Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly			
1210	1215	1220	
gga gag gtc ggc cat cac cgc cct tct gtg ata cct cgc ggc aat cct			3749
Gly Glu Val Gly His His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro			
1225	1230	1235	
gat cag aac ctc ggg act cta cag gcc ttt ccg ccg tca tgt cag atc			3797
Asp Gln Asn Leu Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile			
1240	1245	1250	
agt gct tac cat cag ttg gct gag gaa cta ggt cat cgc ccg gcc cct			3845
Ser Ala Tyr His Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro			
1255	1260	1265	1270
gtc gcc ggc gtc ttg ccc cct tgc cct gag ctt gag cag ggc ctg ctc			3893
Val Ala Ala Val Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu			

	1275	1280	1285	
tat atg cca caa gaa ctt act gtg tcc gat agc gtg ctg gtt ttt gag Tyr Met Pro Gln Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu	1290	1295	1300	3941
ctt acg gat ata gtc cac tgc cgt atg gcc cca agc cag cga aag Leu Thr Asp Ile Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys	1305	1310	1315	3989
gct gtt ctc tca acg ctt gtg ggg agg tac ggc cgt agg act aaa tta Ala Val Leu Ser Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu	1320	1325	1330	4037
tat gag gcg gcg cat tca gat gtc cgt gag tcc cta gcg agg ttt atc Tyr Glu Ala Ala His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile	1335	1340	1345	4085
ccc acc atc ggg cct gtt cg <sup>g</sup> gct acc aca tgt gag ctg tac gag ctg Pro Thr Ile Gly Pro Val Arg Ala Thr Thr Cys Glu Leu Tyr Glu Leu	1355	1360	1365	4133
gtt gaa gcc atg gta gag aag ggt cag gac gga tct gcc gtc cta gag Val Glu Ala Met Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu	1370	1375	1380	4181
ctc gac ctt tgc aat cgt gac gtc tcg cgc atc aca ttt ttc caa aag Leu Asp Leu Cys Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys	1385	1390	1395	4229
gat tgc aat aag ttt aca act ggt gag act atc gcc cat ggc aag gtt Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val	1400	1405	1410	4277
ggc cag ggc ata tcg gcc tgg agc aag acc ttc tgt gct ctg ttt ggc Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly	1415	1420	1425	4325
ccg tgg ttc cgc gcc att gaa aag gaa ata ttg gcc cta ctc ccg cct Pro Trp Phe Arg Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro	1435	1440	1445	4373
aat atc ttt tat ggc gac gcc tat gag gag tca gtg ttt gct gcc gct Asn Ile Phe Tyr Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Ala	1450	1455	1460	4421
gtg tcc ggg gca ggg tca tgt atg gta ttt gaa aat gac ttc tca gag Val Ser Gly Ala Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu	1465	1470	1475	4469
ttt gac agt acc cag aat aat ttc tct ctc ggc ctt gag tgt gtg gtt Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val	1480	1485	1490	4517
atg gag gag tgc ggc atg ccc caa tgg tta att agg ttg tac cat ctg Met Glu Glu Cys Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu	1495	1500	1505	4565
			1510	

gtc cggtca gcc tgg att ttg cag gcg ccg aag gag tct ctt aag ggg Val Arg Ser Ala Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly 1515 1520 1525	4613
ttt tgg aag aag cac tct ggt gag cct ggt acc ctt ctc tgg aac act Phe Trp Lys Lys His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr 1530 1535 1540	4661
gtc tgg aac atg gcg att ata gca cat tgc tay gag ttc cgt gac ttt Val Trp Asn Met Ala Ile Ile Ala His Cys Xaa Glu Phe Arg Asp Phe 1545 1550 1555	4709
cgt gtt gcc gcc ttc aag ggt gat gat tca gtg gtc ctc tgt agt gac Arg Val Ala Ala Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp 1560 1565 1570	4757
tac cga cag rgc cgt aac gcg gct gcc tta att gca ggc tgt ggg ctc Tyr Arg Gln Xaa Arg Asn Ala Ala Leu Ile Ala Gly Cys Gly Leu 1575 1580 1585 1590	4805
aaa ttg aag gtt gat tac cgc cct atc ggg cta tat gct gga gtg gtg Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val 1595 1600 1605	4853
gtg gcc ccc ggt ttg ggg aca ctg ccc gat gtg gtg cgt ttt gcc ggt Val Ala Pro Gly Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly 1610 1615 1620	4901
cgg tta tct gag aag aat tgg ggc cct ggc ccg gag cgt gct gag cag Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln 1625 1630 1635	4949
ctg cgt ctt gct gtt tgt gat ttc ctt cga ggg ttg acg aat gtt gcg Leu Arg Leu Ala Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala 1640 1645 1650	4997
cag gtc tgt gtt gat gtg tcc cgt gtc tat gga gtt agc ccc ggg Gln Val Cys Val Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly 1655 1660 1665 1670	5045
ctg gta cat aac ctt att ggc atg ctg cag acc att gct gat ggc aag Leu Val His Asn Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys 1675 1680 1685	5093
gcc cac ttt aca gar aat att aaa cct gtg ctt gac ctt aca aat tcc Ala His Phe Thr Xaa Asn Ile Lys Pro Val Leu Asp Leu Thr Asn Ser 1690 1695 1700	5141
atc ata caa cgg gtg gaa tgaataacat gtctttgca tcgccccatgg Ile Ile Gln Arg Val Glu 1705	5189
gatcacc atg cgc cct agg gct gtt ctg ttg ctc ttc gtg ctt ttg Met Arg Pro Arg Ala Val Leu Leu Leu Phe Val Leu Leu 1710 1715 1720	5238

cct atg ctg ccc gcg cca ccg gcc ggc cag ccg tct ggc cgc cgt cgt Pro Met Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg 1725 1730 1735	5286
ggg cgg cgc agc ggc ggt gcc ggc ggt ggt ttc tgg ggt gac agg gtt Gly Arg Arg Ser Gly Gly Gly Phe Trp Gly Asp Arg Val 1740 1745 1750	5334
gat tct cag ccc ttc gcc ctc ccc tat att cat cca acc aac ccc ttc Asp Ser Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe 1755 1760 1765 1770	5382
gcc gcc gat gtc gtt tca caa ccc ggg gct gga act cgc cct cga cag Ala Ala Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln 1775 1780 1785	5430
ccg ccc cgc ccc ctt ggy tcc gct tgg cgt gac cag tcc cag cgc ccc Pro Pro Arg Pro Leu Xaa Ser Ala Trp Arg Asp Gln Ser Gln Arg Pro 1790 1795 1800	5478
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act gcc gtg tca ccg gct cct gac aca gcc cct gta cct gat gtt gac Thr Ala Val Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val Asp 1820 1825 1830	5574
tca cgt ggt gct att ctg cgc cgg cag tac aat ttg tcc acg tcc ccc Ser Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro 1835 1840 1845 1850	5622
ctc acg tca tct gtc gct tcg ggt act aat ttg gtc ctc tat gct gcc Leu Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala 1855 1860 1865	5670
ccg ctg aat ccc ctc ttg cct ctc cag gat ggt acc aac act cat att Pro Leu Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile 1870 1875 1880	5718
atg gct act gag gca tcc aat tat gcc cag tat cgg gtt gtt cga gct Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala 1885 1890 1895	5766
aca atc cgt tat cgc ccg ctg gtg ccg aat gcc gtt ggt ggc tat gcc Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala 1900 1905 1910	5814
att tcc att tct ttc tgg ccc caa act aca act acc cct act tct gtc Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Pro Thr Ser Val 1915 1920 1925 1930	5862
gat atg aat tct att act tcc acy gat gtt agg att ttg gtt cag ccc Asp Met Asn Ser Ile Thr Ser Xaa Asp Val Arg Ile Leu Val Gln Pro 1935 1940 1945	5910
ggt att gcc tcc gag cta gtc atc ccc agt gag cgc ctt cat tac cgt	5958

Gly Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg			
1950	1955	1960	
aat caa ggc tgg cgc tct gtt gag acc acg ggt gtg gct gag gag gag			6006
Asn Gln Gly Trp Arg Ser Val Glu Thr Thr Gly Val Ala Glu Glu Glu			
1965	1970	1975	
gct act tcc ggt ctg gta atg ctt tgc att cat ggc tct cct gtt aat			6054
Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn			
1980	1985	1990	
tcc tac act aat aca cct tac act ggt gcg ctg ggg ctt ctt gat ttt			6102
Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe			
1995	2000	2005	2010
gca cta gag ctt gaa ttt agg aat ttg aca ccc ggg aac acc aac acc			6150
Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr			
2015	2020	2025	
cgt gtt tcc cgg tat acc agc aca gcc cgc cac cgg ctg cgc cgt ggt			6198
Arg Val Ser Arg Tyr Thr Ser Thr Ala Arg His Arg Leu Arg Arg Gly			
2030	2035	2040	
gct gat ggg act gct gag ctt act acc aca gca gcc aca cgt ttc atg			6246
Ala Asp Gly Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe Met			
2045	2050	2055	
aag gac ctg cac ttc gct ggc acg aat ggc gtt ggt gag gtg ggt cgt			6294
Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg			
2060	2065	2070	
ggt atc gcc ctg aca ctg ttc aat ctc gct gat acg ctt ctc ggc ggt			6342
Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly			
2075	2080	2085	2090
tta ccg aca gaa ttg att tcg tcg gct ggg ggc caa ctg ttt tac tcc			6390
Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser			
2095	2100	2105	
cgc ccg gtt gtc tca gcc aat ggc gag cca aca gta aag tta tat aca			6438
Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr			
2110	2115	2120	
tct gtt gag aat gcg cag caa gac aag ggc atc acc att cca cat gat			6486
Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp			
2125	2130	2135	
ata gac ctg ggt gac tcc cgt gtg gtt atc cag gat tat gat aac cag			6534
Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln			
2140	2145	2150	
cay gag caa gac cga cct act ccg tca cct gcc ccc tct cgc ccc ttc			6582
Xaa Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe			
2155	2160	2165	2170
tca gtt ctt cgt gcc aat gat gtt ttg tgg ctt tcc ctc act gcc gct			6630
Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala			

2175	2180	2185	
gag tat gac cag act acg tat ggg tcg tcc acc aac cct atg tat gtc Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val 2190			6678
2195			2200
tct gac aca gtt acg ctt gtt aat gtg gct act ggt gct cag gct gtt Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val 2205			6726
2210			2215
gcc cgc tcc ctt gat tgg tct aaa gtt act ctg gac ggc cgc ccc ctt Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu 2220			6774
2225			2230
act acc att cag cag tat tct aag aca ttt tat gtt ctc ccc ctc cgc Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg 2235			6822
2240			2245
2250			
ggg aag ctg tcc ttt tgg gag gct ggc acg act aag gcc ggc tac cct Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro 2255			6870
2260			2265
tac aat tat aat act acc gct agt gac caa att ttg att gag aat gcg Tyr Asn Tyr Asn Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala 2270			6918
2275			2280
gcc ggc cac cgt gtc gct att tcc acc tat acc act agc tta ggt gcc Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Ser Leu Gly Ala 2285			6966
2290			2295
ggt cct acc tcg atc tct gcg gtc ggc gta ctg gct cca cac tct gcc Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala 2300			7014
2305			2310
ctt gcc gtt ctt gag gat act att gat tac ccc gcc cgt gcc cat act Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr 2315			7062
2320			2325
2330			
ttt gat gat ttt tgc ccg gag tgc cgt acc cta ggt ttg cag ggt tgt Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys 2335			7110
2340			2345
gca ttc cag tct act att gct gag ctc cag cgt tta aaa atg aag gta Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val 2350			7158
2355			2360
ggt aaa acc cgg gag tct taattaattc cttctgtgcc cccttcgttag Gly Lys Thr Arg Glu Ser 2365			7206
tttcttcgc ttttatttct tatttctgct ttccgcgctc cctggaaaaa aaaaaaaaaa aaaaaaaaaa a			7266
			7277
<210> 166			
<211> 1708			
<212> PRT			
<213> Hepatitis E Virus			

<220>  
 <223> Xaa = Unknown or Other at position 322  
 <223> Xaa = Unknown or Other at position 331  
 <223> Xaa = Unknown or Other at position 445  
 <223> Xaa = Unknown or Other at position 448  
 <223> Xaa = Unknown or Other at position 634  
 <223> Xaa = Unknown or Other at position 646  
 <223> Xaa = Unknown or Other at position 811  
 <223> Xaa = Unknown or Other at position 1553  
 <223> Xaa = Unknown or Other at position 1578  
 <223> Xaa = Unknown or Other at position 1691  
  
 <400> 166  
 Met Glu Ala His Gln Phe Ile Lys Ala Pro Gly Ile Thr Thr Ala Ile  
 1 5 10 15  
 Glu Gln Ala Ala Leu Ala Ala Asn Ser Ala Leu Ala Asn Ala Val  
 20 25 30  
 Val Val Arg Pro Phe Leu Ser Arg Val Gln Thr Glu Ile Leu Ile Asn  
 35 40 45  
 Leu Met Gln Pro Arg Gln Leu Val Phe Arg Pro Glu Val Leu Trp Asn  
 50 55 60  
 His Pro Ile Gln Arg Val Ile His Asn Glu Leu Glu Gln Tyr Cys Arg  
 65 70 75 80  
 Ala Arg Ala Gly Arg Cys Leu Glu Val Gly Ala His Pro Arg Ser Ile  
 85 90 95  
 Asn Asp Asn Pro Asn Val Leu His Arg Cys Phe Leu Arg Pro Val Gly  
 100 105 110  
 Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro Thr Arg Gly Pro Ala Ala  
 115 120 125  
 Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu Pro Pro Val Asp Arg Thr  
 130 135 140  
 Tyr Cys Phe Asp Gly Phe Ser Arg Cys Ala Phe Ala Ala Glu Thr Gly  
 145 150 155 160  
 Val Ala Leu Tyr Ser Leu His Asp Leu Trp Pro Ala Asp Val Ala Glu  
 165 170 175  
 Ala Met Ala Arg His Gly Met Thr Arg Leu Tyr Ala Ala Leu His Leu  
 180 185 190  
 Pro Pro Glu Val Leu Leu Pro Pro Gly Thr Tyr His Thr Thr Ser Tyr  
 195 200 205  
 Leu Leu Ile His Asp Gly Asn Arg Ala Val Val Thr Tyr Glu Gly Asp  
 210 215 220  
 Thr Ser Ala Gly Tyr Asn His Asp Val Ser Ile Leu Arg Ala Trp Ile  
 225 230 235 240  
 Arg Thr Thr Lys Ile Val Gly Asp His Pro Leu Val Ile Glu Arg Val  
 245 250 255  
 Arg Ala Ile Gly Cys His Phe Val Leu Leu Leu Thr Ala Ala Pro Glu  
 260 265 270

Pro Ser Pro Met Pro Tyr Val Pro Tyr Pro Arg Ser Thr Glu Val Tyr  
 275 280 285  
 Val Arg Ser Ile Phe Gly Pro Gly Gly Ser Pro Ser Leu Phe Pro Ser  
 290 295 300  
 Ala Cys Ser Thr Lys Ser Thr Phe His Ala Val Pro Val His Ile Trp  
 305 310 315 320  
 Asp Xaa Leu Met Leu Phe Gly Ala Thr Leu Xaa Asp Gln Ala Phe Cys  
 325 330 335  
 Cys Ser Arg Leu Met Thr Tyr Leu Arg Gly Ile Ser Tyr Lys Val Thr  
 340 345 350  
 Val Gly Ala Leu Val Ala Asn Glu Gly Trp Asn Ala Ser Glu Asp Ala  
 355 360 365  
 Leu Thr Ala Val Ile Thr Ala Ala Tyr Leu Thr Ile Cys His Gln Arg  
 370 375 380  
 Tyr Leu Arg Thr Gln Ala Ile Ser Lys Gly Met Arg Arg Leu Glu Val  
 385 390 395 400  
 Glu His Ala Gln Lys Phe Ile Thr Arg Leu Tyr Ser Trp Leu Phe Glu  
 405 410 415  
 Lys Ser Gly Arg Asp Tyr Ile Pro Gly Arg Gln Leu Gln Phe Tyr Ala  
 420 425 430  
 Gln Cys Arg Arg Trp Leu Ser Ala Gly Phe His Leu Xaa Pro Arg Xaa  
 435 440 445  
 Leu Val Phe Asp Glu Ser Val Pro Cys Arg Cys Arg Thr Phe Leu Lys  
 450 455 460  
 Lys Val Ala Gly Lys Phe Cys Cys Phe Met Arg Trp Leu Gly Gln Glu  
 465 470 475 480  
 Cys Thr Cys Phe Leu Glu Pro Ala Glu Gly Leu Val Gly Asp Gln Gly  
 485 490 495  
 His Asp Asn Glu Ala Tyr Glu Gly Ser Glu Val Asp Pro Ala Glu Pro  
 500 505 510  
 Ala His Leu Asp Val Ser Gly Thr Tyr Ala Val His Gly His Gln Leu  
 515 520 525  
 Glu Ala Leu Tyr Arg Ala Leu Asn Val Pro His Asp Ile Ala Ala Arg  
 530 535 540  
 Ala Ser Arg Leu Thr Ala Thr Val Glu Leu Val Ala Ser Pro Asp Arg  
 545 550 555 560  
 Leu Glu Cys Arg Thr Val Leu Gly Asn Lys Thr Phe Arg Thr Thr Val  
 565 570 575  
 Val Asp Gly Ala His Leu Glu Ala Asn Gly Pro Glu Glu Tyr Val Leu  
 580 585 590  
 Ser Phe Asp Ala Ser Arg Gln Ser Met Gly Ala Gly Ser His Ser Leu  
 595 600 605  
 Thr Tyr Glu Leu Thr Pro Ala Gly Leu Gln Val Lys Ile Ser Ser Asn  
 610 615 620  
 Gly Leu Asp Cys Thr Ala Thr Phe Pro Xaa Gly Gly Ala Pro Ser Ala  
 625 630 635 640  
 Ala Pro Gly Glu Val Xaa Ala Phe Cys Ser Ala Leu Tyr Arg Tyr Asn  
 645 650 655  
 Arg Phe Thr Gln Arg His Ser Leu Thr Gly Gly Leu Trp Leu His Pro  
 660 665 670  
 Glu Gly Leu Leu Gly Ile Phe Pro Pro Phe Ser Pro Gly His Ile Trp  
 675 680 685  
 Glu Ser Ala Asn Pro Phe Cys Gly Glu Gly Thr Leu Tyr Thr Arg Thr  
 690 695 700  
 Trp Ser Thr Ser Gly Phe Ser Ser Asp Phe Ser Pro Pro Glu Ala Ala  
 705 710 715 720  
 Ala Pro Ala Ser Ala Ala Pro Gly Leu Pro Tyr Pro Thr Pro Pro

725	730	735	
Val Ser Asp Ile Trp Val Leu Pro Pro Pro Ser Glu Glu Ser His Val			
740	745	750	
Asp Ala Ala Ser Val Pro Ser Val Pro Glu Pro Ala Gly Leu Thr Ser			
755	760	765	
Pro Ile Val Leu Thr Pro Pro Pro Pro Pro Pro Val Arg Lys Pro			
770	775	780	
Ala Thr Ser Pro Pro Pro Arg Thr Arg Arg Leu Leu Tyr Thr Tyr Pro			
785	790	795	800
Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu Xaa Glu Ser Asp Cys Asp			
805	810	815	
Trp Leu Val Asn Ala Ser Asn Pro Gly His Arg Pro Gly Gly Leu			
820	825	830	
Cys His Ala Phe Tyr Gln Arg Phe Pro Glu Ala Phe Tyr Ser Thr Glu			
835	840	845	
Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr Thr Leu Thr Pro Arg Pro			
850	855	860	
Ile Ile His Ala Val Ala Pro Asp Tyr Arg Val Glu Gln Asn Pro Lys			
865	870	875	880
Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys Ser Arg Arg Gly Thr Ala			
885	890	895	
Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr Gln Val Pro Val Ser Leu			
900	905	910	
Ser Phe Asp Ala Trp Glu Arg Asn His Arg Pro Gly Asp Glu Leu Tyr			
915	920	925	
Leu Thr Glu Pro Ala Ala Ala Trp Phe Glu Ala Asn Lys Pro Ala Gln			
930	935	940	
Pro Ala Leu Thr Ile Thr Glu Asp Thr Ala Arg Thr Ala Asn Leu Ala			
945	950	955	960
Leu Glu Ile Asp Ala Ala Thr Glu Val Gly Arg Ala Cys Ala Gly Cys			
965	970	975	
Thr Ile Ser Pro Gly Ile Val His Tyr Gln Phe Thr Ala Gly Val Pro			
980	985	990	
Gly Ser Gly Lys Ser Arg Ser Ile Gln Gln Gly Asp Val Asp Val Val			
995	1000	1005	
Val Val Pro Thr Arg Glu Leu Arg Asn Ser Trp Arg Arg Arg Gly Phe			
1010	1015	1020	
Ala Ala Phe Thr Pro His Thr Ala Ala Arg Val Thr Ile Gly Arg Arg			
1025	1030	1035	1040
Val Val Ile Asp Glu Ala Pro Ser Leu Pro Pro His Leu Leu Leu			
1045	1050	1055	
His Met Gln Arg Ala Ser Ser Val His Leu Leu Gly Asp Pro Asn Gln			
1060	1065	1070	
Ile Pro Ala Ile Asp Phe Glu His Ala Gly Leu Val Pro Ala Ile Arg			
1075	1080	1085	
Pro Glu Leu Ala Pro Thr Ser Trp Trp His Val Thr His Arg Cys Pro			
1090	1095	1100	
Ala Asp Val Cys Glu Leu Ile Arg Gly Ala Tyr Pro Lys Ile Gln Thr			
1105	1110	1115	1120
Thr Ser Arg Val Leu Arg Ser Leu Phe Trp Asn Glu Pro Ala Ile Gly			
1125	1130	1135	
Gln Lys Leu Val Phe Thr Gln Ala Ala Lys Ala Ala Asn Pro Gly Ala			
1140	1145	1150	
Ile Thr Val His Glu Ala Gln Gly Ala Thr Phe Thr Glu Thr Thr Ile			
1155	1160	1165	
Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile Gln Ser Ser Arg Ala His			
1170	1175	1180	

Ala Ile Val Ala Leu Thr Arg His Thr Glu Lys Cys Val Ile Leu Asp  
 1185 1190 1195 1200  
 Ala Pro Gly Leu Leu Arg Glu Val Gly Ile Ser Asp Val Ile Val Asn  
 1205 1210 1215  
 Asn Phe Phe Leu Ala Gly Gly Glu Val Gly His His Arg Pro Ser Val  
 1220 1225 1230  
 Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu Gly Thr Leu Gln Ala Phe  
 1235 1240 1245  
 Pro Pro Ser Cys Gln Ile Ser Ala Tyr His Gln Leu Ala Glu Glu Leu  
 1250 1255 1260  
 Gly His Arg Pro Ala Pro Val Ala Ala Val Leu Pro Pro Cys Pro Glu  
 1265 1270 1275 1280  
 Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln Glu Leu Thr Val Ser Asp  
 1285 1290 1295  
 Ser Val Leu Val Phe Glu Leu Thr Asp Ile Val His Cys Arg Met Ala  
 1300 1305 1310  
 Ala Pro Ser Gln Arg Lys Ala Val Leu Ser Thr Leu Val Gly Arg Tyr  
 1315 1320 1325  
 Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala His Ser Asp Val Arg Glu  
 1330 1335 1340  
 Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly Pro Val Arg Ala Thr Thr  
 1345 1350 1355 1360  
 Cys Glu Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp  
 1365 1370 1375  
 Gly Ser Ala Val Leu Glu Leu Asp Leu Cys Asn Arg Asp Val Ser Arg  
 1380 1385 1390  
 Ile Thr Phe Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr  
 1395 1400 1405  
 Ile Ala His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr  
 1410 1415 1420  
 Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Glu Ile  
 1425 1430 1435 1440  
 Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr Gly Asp Ala Tyr Glu Glu  
 1445 1450 1455  
 Ser Val Phe Ala Ala Ala Val Ser Gly Ala Gly Ser Cys Met Val Phe  
 1460 1465 1470  
 Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu  
 1475 1480 1485  
 Gly Leu Glu Cys Val Val Met Glu Glu Cys Gly Met Pro Gln Trp Leu  
 1490 1495 1500  
 Ile Arg Leu Tyr His Leu Val Arg Ser Ala Trp Ile Leu Gln Ala Pro  
 1505 1510 1515 1520  
 Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys His Ser Gly Glu Pro Gly  
 1525 1530 1535  
 Thr Leu Leu Trp Asn Thr Val Trp Asn Met Ala Ile Ile Ala His Cys  
 1540 1545 1550  
 Xaa Glu Phe Arg Asp Phe Arg Val Ala Ala Phe Lys Gly Asp Asp Ser  
 1555 1560 1565  
 Val Val Leu Cys Ser Asp Tyr Arg Gln Xaa Arg Asn Ala Ala Leu  
 1570 1575 1580  
 Ile Ala Gly Cys Gly Leu Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly  
 1585 1590 1595 1600  
 Leu Tyr Ala Gly Val Val Val Ala Pro Gly Leu Gly Thr Leu Pro Asp  
 1605 1610 1615  
 Val Val Arg Phe Ala Gly Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly  
 1620 1625 1630  
 Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala Val Cys Asp Phe Leu Arg

1635	1640	1645	
Gly Leu Thr Asn Val Ala Gln Val Cys Val Asp Val Val Ser Arg Val			
1650	1655	1660	
Tyr Gly Val Ser Pro Gly Leu Val His Asn Leu Ile Gly Met Leu Gln			
1665	1670	1675	
Thr Ile Ala Asp Gly Lys Ala His Phe Thr Xaa Asn Ile Lys Pro Val		1680	
1685	1690	1695	
Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg Val Glu			
1700	1705		
<210> 167			
<211> 660			
<212> PRT			
<213> Hepatitis E Virus			
<220>			
<223> Xaa = Unknown or Other at position 84			
<223> Xaa = Unknown or Other at position 230			
<223> Xaa = Unknown or Other at position 447			
<400> 167			
Met Arg Pro Arg Ala Val Leu Leu Leu Phe Val Leu Leu Pro Met			
1	5	10	15
Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg			
20	25	30	
Arg Ser Gly Gly Ala Gly Gly Phe Trp Gly Asp Arg Val Asp Ser			
35	40	45	
Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala			
50	55	60	
Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro			
65	70	75	80
Arg Pro Leu Xaa Ser Ala Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala			
85	90	95	
Ala Pro Arg Arg Ser Ala Pro Ala Gly Ala Ala Pro Leu Thr Ala			
100	105	110	
Val Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg			
115	120	125	
Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr			
130	135	140	
Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu			
145	150	155	160
Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala			
165	170	175	
Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile			
180	185	190	
Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser			
195	200	205	
Ile Ser Phe Trp Pro Gln Thr Thr Pro Thr Ser Val Asp Met			
210	215	220	
Asn Ser Ile Thr Ser Xaa Asp Val Arg Ile Leu Val Gln Pro Gly Ile			
225	230	235	240
Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln			
245	250	255	
Gly Trp Arg Ser Val Glu Thr Thr Gly Val Ala Glu Glu Ala Thr			
260	265	270	

Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr  
 275 280 285  
 Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu  
 290 295 300  
 Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val  
 305 310 315 320  
 Ser Arg Tyr Thr Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp  
 325 330 335  
 Gly Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe Met Lys Asp  
 340 345 350  
 Leu His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile  
 355 360 365  
 Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro  
 370 375 380  
 Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
 385 390 395 400  
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 405 410 415  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp  
 420 425 430  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln Xaa Glu  
 435 440 445  
 Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val  
 450 455 460  
 Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr  
 465 470 475 480  
 Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp  
 485 490 495  
 Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg  
 500 505 510  
 Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr  
 515 520 525  
 Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys  
 530 535 540  
 Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn  
 545 550 555 560  
 Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly  
 565 570 575  
 His Arg Val Ala Ile Ser Thr Tyr Thr Ser Leu Gly Ala Gly Pro  
 580 585 590  
 Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala  
 595 600 605  
 Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp  
 610 615 620  
 Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe  
 625 630 635 640  
 Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys  
 645 650 655  
 Thr Arg Glu Ser  
 660

<210> 168  
 <211> 122  
 <212> PRT  
 <213> Hepatitis E Virus

<220>

<223> us2 orf3

<223> Xaa = Unknown or Other at position 97

<400> 168

Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys	Ala	Leu
1					5				10					15	
Gly	Leu	Phe	Cys	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys	Pro	Arg
					20				25					30	
His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Ala	Ala	Ala
					35				40					45	
Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser	Pro	Ser
					50				55					60	
Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met	Ser	Phe
					65				70					80	
His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala	Pro	Leu
					85				90					95	
Xaa	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro	Pro	Val
					100				105					110	
Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg						
					115				120						

<210> 169

<211> 33

<212> PRT

<213> Hepatitis E Virus

<220>

<223> M 4-2

<400> 169

Ala	Asn	Gln	Pro	Gly	His	Leu	Ala	Pro	Leu	Gly	Glu	Ile	Arg	Pro	Ser
1					5				10					15	
Ala	Pro	Pro	Leu	Pro	Pro	Val	Ala	Asp	Leu	Pro	Gln	Pro	Gly	Leu	Arg
					20				25					30	
Arg															

<210> 170

<211> 48

<212> PRT

<213> Hepatitis E Virus

<220>

<223> M 3-2e

<400> 170

Thr	Phe	Asp	Tyr	Pro	Gly	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1						5			10					15	
Glu	Cys	Arg	Ala	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Val
						20			25					30	
Ala	Glu	Leu	Gln	Arg	Leu	Lys	Val	Lys	Val	Gly	Lys	Thr	Arg	Glu	Leu
						35			40					45	

<210> 171

<211> 33

<212> PRT

<213> Hepatitis E Virus  
 <220>  
 <223> B 4-2

<400> 171  
 Ala Asn Pro Pro Asp His Ser Ala Pro Leu Gly Val Thr Arg Pro Ser  
 1 5 10 15  
 Ala Pro Pro Leu Pro His Val Val Asp Leu Pro Gln Leu Gly Pro Arg  
 20 25 30  
 Arg

<210> 172  
 <211> 48  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> B 3-2e

<400> 172  
 Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro  
 1 5 10 15  
 Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val  
 20 25 30  
 Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Leu  
 35 40 45

<210> 173  
 <211> 33  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> OFR3 (u4.2)

<400> 173  
 Asp Ser Arg Pro Ala Pro Ser Val Pro Leu Gly Val Thr Ser Pro Ser  
 1 5 10 15  
 Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg  
 20 25 30  
 Arg

<210> 174  
 <211> 48  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> ORF2 (u3.2e)

<400> 174  
 Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro  
 1 5 10 15  
 Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile

20	25	30	
Ala Glu Leu Gln Arg Leu Lys Met	Lys Val Gly Lys Thr Arg Glu Ser		
35	40	45	
<210> 175			
<211> 327			
<212> PRT			
<213> Hepatitis E Virus			
<220>			
<223> US-1 SG3			
<223> Xaa = Unknown or Other at position 148			
<223> Xaa = Unknown or Other at position 209			
<223> Xaa = Unknown or Other at position 262			
<400> 175			
Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe			
1	5	10	15
Met Lys Asp Leu His Phe Thr Gly Thr Asn Gly Val Gly Glu Val Gly			
20	25	30	
Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly			
35	40	45	
Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr			
50	55	60	
Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr			
65	70	75	80
Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His			
85	90	95	
Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn			
100	105	110	
Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro			
115	120	125	
Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala			
130	135	140	
Ala Glu Tyr Xaa Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr			
145	150	155	160
Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala			
165	170	175	
Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro			
180	185	190	
Leu Thr Thr Ile Gln Gln Tyr Ser Lys Lys Phe Tyr Val Leu Pro Leu			
195	200	205	
Xaa Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr			
210	215	220	
Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn			
225	230	235	240
Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Ser Leu Gly			
245	250	255	
Ala Gly Pro Thr Ser Xaa Ser Ala Val Gly Val Leu Ala Pro His Ser			
260	265	270	
Ala Leu Ala Val Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His			
275	280	285	
Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly			
290	295	300	

Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys  
 305 310 315 320  
 Val Gly Lys Thr Arg Glu Ser  
 325

<210> 176  
 <211> 327  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> US-2 SG3

<223> Xaa = Unknown or Other at position 114

<400> 176  
 Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe  
 1 . 5 10 15  
 Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly  
 20 25 30  
 Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly  
 35 40 45  
 Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr  
 50 55 60  
 Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr  
 65 70 75 80  
 Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His  
 85 90 95  
 Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn  
 100 105 110  
 Gln Xaa Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro  
 115 120 125  
 Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala  
 130 135 140  
 Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr  
 145 150 155 160  
 Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala  
 165 170 175  
 Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro  
 180 185 190  
 Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu  
 195 200 205  
 Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr  
 210 215 220  
 Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn  
 225 230 235 240  
 Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Ser Leu Gly  
 245 250 255  
 Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser  
 260 265 270  
 Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His  
 275 280 285  
 Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly  
 290 295 300  
 Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys  
 305 310 315 320  
 Val Gly Lys Thr Arg Glu Ser

325

<210> 177		
<211> 21		
<212> DNA		
<213> Hepatitis E Virus		
<220>		
<223> HEVConsORF1-s2		
<400> 177		
ctgccytkgc gaatgctgtg g	21	
<210> 178		
<211> 24		
<212> DNA		
<213> Hepatitis E Virus		
<220>		
<223> HEVConsORF1-a2		
<400> 178		
ggcagwrtac carcgctgaa catc	24	
<210> 179		
<211> 294		
<212> DNA		
<213> Hepatitis E Virus		
<220>		
<223> z12-orf1 (G.S.)		
<400> 179		
tggcattact actgccattg agcaagctgc tctggctgctg gccaattctg ccttggcgaa	60	
tgctgtggtg gtcggccgt ttttatctcg ttacagact gagattctta ttaatttgat	120	
gcaaccccgaa cagttggctt ttgcacctga ggtgttctgg aaccatccca tccaaacgtgt	180	
tatacataat gaattggagc agtactgccc ggcggggcc ggtcgctgtc tggaaattgg	240	
agcccatcca agtcaatca atgataatcc taatgttctg catcggttt tcct	294	
<210> 180		
<211> 418		
<212> DNA		
<213> Hepatitis E Virus		
<220>		
<223> z12-orf1.con		
<400> 180		
ctggcattac tactgctatt gagcaagctg ctctgggtgc ggccaattct gccttggcgaa	60	
atgctgtggt gttcgccgt ttttatctc ttacagac tgagattctt attaatttgat	120	
tgcaaccccg acaagttggtc ttgcacctg aggtgttctg gaaccatccc atccaaacgtgt	180	
ttatacataa tgaattggag cagtactgcc gggccgggc cggcgctgt ctggaaatttg	240	
gagcccatcc aaggtaatc aatgataatc ctaatgttct gcattcggtgc tttttacgac	300	
cggtcgggag ggacgttcag cgctggtact ccggccac ccgtggccc gcggccaaact	360	
ccgcgggtc tgcgtgcgt ggtctccccc ctgtcgaccg cacttactgc ctcgatgg	418	
<210> 181		

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<211> 197
<212> DNA
<213> Hepatitis E Virus

<220>
<223> z12-orf2.con

<400> 181
gacagaatta atttcgtcgg ctgggggtca actgttctac tcccgccctg tcgtctcagc      60
caatggcgag ccgactgtca agttatacac acatgttgag aatgcacagc aggataaggg      120
gatagttattt ccacatgaca tagatttggg cgactctcgt ttggtaatcc aggattatga      180
taaccaacac gaacaag      197

<210> 182
<211> 25
<212> DNA
<213> Hepatitis E Virus

<220>
<223> HEVConsORF2/3-s1

<400> 182
gtatcgkkyk gaatgaataa catgt      25

<210> 183
<211> 25
<212> DNA
<213> Hepatitis E Virus

<220>
<223> HEVConsORF2/3-a1

<400> 183
aggggttggg tgatgaata taggg      25

<210> 184
<211> 234
<212> DNA
<213> Hepatitis E Virus

<220>
<223> z12.orf23.con

<400> 184
gtatcgktt gaatgaataa catgtttgt gcatcgccca tgggatcacc atgcgcctta      60
gggttggtct gttgttggtc ctctgtttc tgcctatgct gcccgcgcca ccggccggcc      120
agycgactgg ccgcgcgtcg gggcggcgca gcggcgggtgc cggcgggtgg ttctggggtg      180
acagggttga ttctcagccc ttgcgcctcc cctatattca tccaaccaac ccct      234

<210> 185
<211> 890
<212> DNA
<213> Hepatitis E Virus

<220>
<223> z12-3p.race

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<400> 185  
 gtcgtctcg ccaatggcg a gccgactgtc a agttataca catctgttga gaatgcacag 60  
 caggataagg gtagatgtat tccacatgac atagattgg gtagactctcg tttggtaatc 120  
 caggattacg ataattcagca cgagcaggac cggcccaccc cttcgccgc cccgtctcg 180  
 ctttcgtt ctcctccgcg taatgtatgt ttgtggctt ctcttaccgc tgctgagtt 240  
 gaccagacta catatgggtc gtccaccaac ccgatgtatg tctcagacac tgatcattt 300  
 gtcaatgtgg ccacaggggc tcaggtgtc gcccgttctc ttgattggc taaagtacc 360  
 ctggacggcc gcccttttac taccatccag cagtagtcta agacattttt tggctccca 420  
 cttcgcggga agttatctt ttgggaggct ggcacaacta aagccggta cccttataat 480  
 tataacacaa ctgcttagtga ccagattctg attgaaaacg cggctggcca tcgtgtcg 540  
 atatctactt atactactag cctggcgcc gcccgtgtt cagtttctgc ggttgggtg 600  
 ttagccac actcgagccct tgctattctt gaagacactg ttgactatcc gggccgtgct 660  
 cacactttt atgacttctg tccgaatgc cgtccctgg gtcgcagggt gttgtgtttt 720  
 caatctacta tcgctgagct ccagcgtctt aaaatgaagg tagcaaaac cggggagttt 780  
 taattaaattc ttcttgcgc cccttcacgg ttctcgctt attctttct tctgcctccc 840  
 gcgctccctg gaaaaaaaaaaaaaaa aaaaaaaaaaaa gtactagtcg acgcgtggcc 890

<210> 186  
 <211> 919  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> z12-3p.con

<400> 186  
 gacagaatta atttcgtcg ctgggggtca actgttctac tcccgccctg tcgtctcagc 60  
 caatggcgag ccgactgtca agttatacac atctgtttag aatgcacagc aggataaggg 120  
 gatagctatt ccacatgaca tagatttggg cgactctcg tggtaatcc aggattacga 180  
 taatcagcac gaggcaggacc ggcccacccc ttccggccgc ccgtctcg 240  
 cctccgcgt aatgtatgtt tggcttcc tcttaccgct gctgagttt accagactac 300  
 atatgggtcg tccaccaacc cgatgtatgt ctcagacact gttacattt tcaatgtggc 360  
 cacaggggct caggctgtcg cccgtctct tgattggctt aaagttaccc tggacggccg 420  
 ccctctact accatccagc agtactctaa gacattttt gttctccac ttccggaa 480  
 gttatcttt tggaggctg gcacaactaa agccggttac cttataatt ataacacaac 540  
 tgcttagtgc cagattctga ttgaaaacgc ggctggccat cgtgtcgcta tatctactta 600  
 tactactagc ctggcgccg gcccgtgtc agtttctgct gttgggtgt tagccccaca 660  
 ctccggccctt gctattctt aagacactgt tgactatccg gcccgtgctc acactttga 720  
 tgacttctgt ccgaatgc gtcgcctggg tctgcagggt tggcttttc aatctactat 780  
 cgctgagctc cagcgtctt aaatgaaggt aggccaaaacc cggggagttt aattaattct 840  
 tcttgcgc cccttcacggt tctcgcttta ttctttctt ctgcctcccg cgctccctgg 900  
 aaaaaaaaaaaaaaaa aaaaaaaaaaaa 919

<210> 187  
 <211> 138  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> z12-orf1.pep

<400> 187  
 Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Gly Ala Ala Asn Ser  
 1 5 10 15  
 Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Leu Gln  
 20 25 30  
 Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg

35	40	45
Pro Glu Val Phe Trp Asn His	Pro Ile Gln Arg Val	Ile His Asn Glu
50	55	60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala	Gly Arg Cys Leu Glu Ile Gly	
65	70	75
Ala His Pro Arg Ser Ile Asn Asp Asn	Pro Asn Val Leu His Arg Cys	
85	90	95
Phe Leu Arg Pro Val Gly Arg Asp Val	Gln Arg Trp Tyr Ser Ala Pro	
100	105	110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala	Leu Arg Gly Leu	
115	120	125
Pro Pro Val Asp Arg Thr Tyr Cys Leu Asp		
130	135	

<210> 188  
 <211> 61  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> z12-orf2-5'.pep

<223> Xaa = Unknown or Other at position 25

1	5	10	15
Leu Pro Ala Pro Pro Ala Gly Gln Xaa	Thr Gly Arg Arg Gly Arg		
20	25	30	
Arg Ser Gly Gly Ala Gly Gly Phe Trp Gly Asp Arg	Val Asp Ser		
35	40	45	
Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro			
50	55	60	

<210> 189  
 <211> 276  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> z12-orf2-3'.pep

1	5	10	15
Val Val Ser Ala Asn Gly Glu Pro Thr Val	Lys Leu Tyr Thr Ser Val		
20	25	30	
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp			
35	40	45	
Leu Gly Asp Ser Arg Leu Val Ile Gln Asp Tyr Asp Asn Gln His Glu			
50	55	60	
Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val			
65	70	75	80
Leu Arg Ala Asn Asp Ala Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr			
85	90	95	
Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp			
100	105	110	

Thr Val Thr Phe Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg  
 115 120 125  
 Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr  
 130 135 140  
 Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys  
 145 150 155 160  
 Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn  
 165 170 175  
 Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly  
 180 185 190  
 His Arg Val Ala Ile Ser Thr Tyr Thr Ser Leu Gly Ala Gly Pro  
 195 200 205  
 Val Ser Val Ser Ala Val Gly Val Leu Ala Pro His Ser Ser Leu Ala  
 210 215 220  
 Ile Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp  
 225 230 235 240  
 Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe  
 245 250 255  
 Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys  
 260 265 270  
 Thr Arg Glu Phe  
 275

<210> 190  
 <211> 74  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> z12-orf3.pep

<400> 190  
 Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu  
 1 5 10 15  
 Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg  
 20 25 30  
 His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala  
 35 40 45  
 Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser  
 50 55 60  
 Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro  
 65 70

<210> 191  
 <211> 408  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> pJOorf3-29.seq

<400> 191  
 gaattcatga ataacatgtc ttttgcacatcg cccatgggat caccatgcgc cctagggtcg 60  
 ttctgttgtt gctcttcgtg cttttgccta tgctgcccgc gccaccggcc agccagccgt 120  
 ctggccgcgg tcgtgggcgg cgccagccgc gtgccggcg tggttctgg ggtgacaggg 180  
 ttgattctca gcccttcgccc cttccctata ttcatccaac caacccttc gccgcccgtg 240  
 tcgtttcaca acccggggct ggaactcgcc ctcgacagcc gccccggccc cttggctccg 300

cttggcgtga ccagtcccag cgccccctccg ctgccccccg tcgtcgatct gccccagctt	360
ggtctgcgcc gcgactacaa ggacgacgat gacaagtaat aaggatcc	408
<210> 192	
<211> 1026	
<212> DNA	
<213> Hepatitis E Virus	
<220>	
<223> cksorf2m-2.seq	
<400> 192	
gaattcatgg gtgctgtatgg gactgctgag cttactacca cagcagccac acgtttcatg	60
aaggacactgc acttcgctgg cacgaatggc gttgggtgagg tgggtcggtgg ttcgcctcg	120
acactgttca atctcgctga tacgcttctc ggcgggttac cgacagaatt gatggcgatcg	180
gctggggcc aactgtttta ctcccggccg gttgtctcg ccaatggcgaa gccaacagta	240
aagttatata catctgttga gaatgcgcag caagacaagg gcatcaccat tccacatgtat	300
atagacactgg gtgactcccg tggatgttatac caggattatg ataaccagca tgagcaagac	360
cgacactactc cggtcacccgc cccctctcgcc cccttctcgat ttcttcgtgc caatgtatgtt	420
ttgtggctt ccctcactgc cgctgagttt gaccagacta cgtatgggtc gtccaccaac	480
cctatgtatg tctctgacac agttacgctt gttaatgtgg ctactggcgatcg tcaggctgtt	540
gcccgcctcc ttgattgggtc taaagttact ctggacggcc gccccttac taccattcag	600
cagtattcta agacatttttata tgttctcccg ctccgcggga agctgttccctt ttggaggct	660
ggcacgacta aggccggcta cccttacaat tataataacta ccgtactgtga ccaaatttttgc	720
attgagaatg cgcccgccca ccgtgtcgat atttccaccc ataccactatg cttaggtgcc	780
gttcctaccc cgtatctctgc ggtcgccgtat ctggctccac actctgcctt tgccgttctt	840
gaggatacta ttgattaccctt ccggccgtgcc catacttttgc atgatttttgc cccggagtgc	900
cgtacccatgg gtttgcagggtt ttgtgcatttgc cagtctactat ttgtcgatctt ccagcgatcc	960
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ggatcc	1026
<210> 193	
<211> 1389	
<212> DNA	
<213> Hepatitis E Virus	
<220>	
<223> CKSORF32M-3.seq	
<400> 193	
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ctggcccccgc tcgtggggcg cgtagccgcg gtgcggccgg tgggttctgg ggtgacaggg	180
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tcgtttcaca acccggggctt ggaactcgcc ctcgacagcc gccccggcccc cttggctccg	300
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ggctcgccgc gccgtgtatcgat tggactgtatcgat gagcttacta ccacagcagcc cacacgttcc	420
atgaaggacc tgcacttcgc tggcacgaat ggcgttggat aggtgggtcg tggatcgatcg	480
ctgacactgt tcaatctcgatcgat tgcgtatcgat ctcggccgtt taccgacaga attgatttgc	540
tcggctgggg gccaactgtt ttactccgc ccgggttgcctt cagccaatgg cgagccaaaca	600
gtaaagttat atacatctgt tgagaatgcgc cagcaagaca agggcatcac cattccacat	660
gatatacgacc tgggtgactt ccgtgtggat atccaggattt atgataacca gcatgagcaa	720
gaccgaccta ctccgtcacc tggcccttctt cggcccttctt cagttcttcg tgccaaatgtat	780
gttttgcgtt tttccctcaat tggccgtatcgat tggccgtatcgat tggccgtatcgat gtcgtccacc	840
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gttgcggctt cccttgcgtt gtcataatcgat tggccgtatcgat tggccgtatcgat gtcgtccacc	960
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ttgattgaga atgcggccgg	ccaccgtgtc gctatttcca	cctataaccac tagcttaggt	1140
gccgggtctta cctcgatctc	tgcggtcggtc gtactggctc	cacactctgc cttggcggtt	1200
cttgaggata ctattgatta	ccccggccgt gcccataactt	ttgatgattt ttgcccggag	1260
tgccgtaccc taggtttgca	gggttgtgca ttccagtc	ctattgctga gctccagcgt	1320
ttaaaaatga aggtaggtaa	aaccggggag tctgactaca	aggacgacga tgacaagtaa	1380
taaggatcc			1389

<210> 194  
 <211> 408  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> plorf3-12.con

<400> 194			
gaattcatga ataacatgtc	tttgcacatcg cccatggat	caccatgcgc cctagggtcg	60
ttctgtgtt gctcttcgtg	ctttgccta tgctgcccgc	gccaccggcc ggccagccgt	120
ctggccgcgg tcgtggcg	cgcagggcg gtgcccgg	tgggttctgg ggtgacaggg	180
ttgattctca gcccttcgcc	ctccccata ttcatccaac	caaccccttc gccgcgcgt	240
tcgtttcaca acccggggt	ggaactcgcc ctcgacagcc	gccccggccc cttggctccg	300
cttggcgtga ccagtcccag	cgcgcctccg ctgccccccg	tcgtcgatct gccccagctt	360
ggtctgcgcc	gcaactacaa ggacgacgt	gacaagtaat aaggatcc	408

<210> 195  
 <211> 1026  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> plorf2.2-6.seq

<400> 195			
gaattcatgg gtgctgtatgg	gactgctgag cttactacca	cagcagccac acgtttcatg	60
aaggacctgc acttcgctgg	cacgaatggc gttggtgagg	tgggtcggtt tattcgccctg	120
acactgttca atctcgctga	tacgcttctc ggcggtttac	cgacagaatt gatttcgtcg	180
gctgggggcc aactgttttta	ctcccgccccg gttgtctcag	ccaatggcga gccaacagta	240
aagttatata catctgttga	aatgcgcag caagacaagg	gcatcaccat tccacatgtat	300
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cgacctactc cgtcacctgc	cccctctcgc cccttctcag	ttcttcgtgc caatgtat	420
ttgtggctt ccctcactgc	cgctgagttt gaccagacta	cgtatgggtc gtccaccaac	480
cctatgtatg tctctgacac	agttacgctt gtaatgtgg	ctactgggtc tcaggctgtt	540
gcccgcctcc ttgattgggtc	taaagttact ctggacggcc	gcccccttac taccattcag	600
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ggcacgacta aggccggcta	cccttacaat tataataacta	ccgctagtga ccaaattttg	720
attgagaatg cgccggcca	ccgtgtcgct atttccaccc	ataccactag cttaggtgcc	780
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cgtaccctag gtttgcaggg	ttgtgcattc cagtctacta	ttgctgagct ccagcgttta	960
aaaatgaagg taggtaaaac	ccgggagtct gactacaagg	acgacgatga caagtaataa	1020
ggatcc			1026

<210> 196  
 <211> 1389  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> PLORF32M-14-5.seq

<400> 196

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gaattcatga ataacatgtc ttttgcacatcg cccatggat caccatgcgc cctagggtcg      60
ttctgtgtt gctcttcgtg cttttgccta tgctgcccgc gccaccggcc agccagccgt      120
ctggccgcgc tcgtggggcg cgtagccgcgt gtcggccgg tggtttctgg ggtgacaggg      180
ttgattctca gcccattcgc cttccctata ttcatccaaac caaccccttc gccgcccgtg      240
tcgtttcaca accccggggct ggaactcgcc ctcgacagcc gcccccggcc cttggctccg      300
cttggcgtga ccagtcccaag cggccctccg ctggcccccgt tggctcgatct gccccagctt      360
ggctctgcgc gccggctgtga tgggactgct gagcttacta ccacagcgcg cacacgttcc      420
atgaaggacc tgcacttcgc tggcacgaat ggcgttgggtg aggtgggtcg tggtatcgcc      480
ctgacactgt tcaatctcgc tgatacgtt ctcggcggtt taccgacaga attgatttcg      540
tcggctgggg gccaactgtt ttactccgc cccgggttgc tggccatgg cgagccaaaca      600
gtaaagttat atacatctgt tgagaatgcg cagcaagaca agggcatcac cattccacat      660
gatatagacc tgggtgactc ccgtgtgggtt atccaggatt atgataacca gcatgagcaa      720
gaccgaccta cttccgtcacc tgccccctct cggccctctt cagttcttcg tgccaaatgat      780
gttttgcgttgc ttccctcacc tgccgtgtgag tatgaccaga ctacgtatgg gtcgtccacc      840
aaccctatgt atgtctctga cacagttacg cttgttaatg tggctactgg tgctcaggct      900
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cagcagtatt ctaagacatt ttatgttctc cccgtccgcg ggaagctgtc cttttgggag      1020
gctggcacga ctaaggccgg ctacccttac aattataata ctaccgcttag tgaccaaatt      1080
ttgatttgaga atgcggccgg ccaccgtgtc gctatttcca cctataaccac tagcttaggt      1140
gcccgtcccta cctcgatctc tgccgtcggtc gtactggctc cacactctgc cttggccgtt      1200
cttgaggata ctattgatta ccccgccccgt gcccataactt ttgatgatt ttgcccggag      1260
tgccgtaccc taggtttgca ggggttgc ttcagttctaa ctattgctga gctccagcgt      1320
ttaaaaatga aggttaggtaa aaccggggag tctgactaca aggacgacga tgacaagtaa      1380
taaggatcc      1389
  
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<210> 197  
 <211> 74  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> z12-orf3-5'.pep

<223> Xaa = Unknown or Other at position 37

<400> 197

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Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
      1           5           10           15
Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
      20          25           30
His Arg Pro Ala Xaa Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala
      35          40           45
Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
      50          55           60
Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro
      65          70
  
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<210> 198  
 <211> 63  
 <212> DNA  
 <213> Hepatitis E Virus

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<220>
<223> Primer orf23p

<400> 198
tatatggatc ctattactt gtcatcgatc tcctttagt cagactcccg ggtttacct      60
acc                                         63

<210> 199
<211> 338
<212> PRT
<213> Hepatitis E Virus

<220>
<223> cksorf2m-2.pep

<400> 199
Glu Phe Met Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala
 1           5           10          15
Thr Arg Phe Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly
 20          25          30
Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr
 35          40          45
Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln
 50          55          60
Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val
 65          70          75          80
Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr
 85          90          95
Ile Pro His Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp
100         105         110
Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro
115         120         125
Ser Arg Pro Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser
130         135         140
Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn
145         150         155         160
Pro Met Tyr Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly
165         170         175
Ala Gln Ala Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp
180         185         190
Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val
195         200         205
Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys
210         215         220
Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu
225         230         235         240
Ile Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr
245         250         255
Ser Leu Gly Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala
260         265         270
Pro His Ser Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala
275         280         285
Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly
290         295         300
Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu
305         310         315         320
Lys Met Lys Val Gly Lys Thr Arg Glu Ser Asp Tyr Lys Asp Asp Asp

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325	330	335
Asp Lys		
<pre> &lt;210&gt; 200 &lt;211&gt; 338 &lt;212&gt; PRT &lt;213&gt; Hepatitis E Virus  &lt;220&gt; &lt;223&gt; plorf2.2-6.pep  &lt;400&gt; 200 Glu Phe Met Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala  1           5           10          15 Thr Arg Phe Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly  20          25          30 Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr  35          40          45 Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln  50          55          60 Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val  65          70          75          80 Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr  85          90          95 Ile Pro His Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp 100          105         110 Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro 115          120         125 Ser Arg Pro Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser 130          135         140 Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn 145          150         155          160 Pro Met Tyr Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly 165          170         175 Ala Gln Ala Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp 180          185         190 Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val 195          200         205 Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys 210          215         220 Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu 225          230         235          240 Ile Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr 245          250         255 Ser Leu Gly Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala 260          265         270 Pro His Ser Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala 275          280         285 Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly 290          295         300 Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu 305          310         315          320 Lys Met Lys Val Gly Lys Thr Arg Glu Ser Asp Tyr Lys Asp Asp Asp 325          330         335 Asp Lys </pre>		

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<210> 201
<211> 37
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Primer orf35p

<400> 201
tatatgaatt catgaataac atgtcttttg catcgcc 37

<210> 202
<211> 68
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Primer orf33p

<400> 202
tatatggatc cttattactt gtcatcgatcg tcctttagt cgccgcgcag accaagctgg 60
ggcagatc 68

<210> 203
<211> 132
<212> PRT
<213> Hepatitis E Virus

<220>
<223> pJOorf3-29.pep

<400> 203
Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
1 5 10 15
Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys
20 25 30
Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala
35 40 45
Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser
50 55 60
Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met
65 70 75 80
Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala
85 90 95
Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro
100 105 110
Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp
115 120 125
Asp Asp Asp Lys
130

<210> 204
<211> 132
<212> PRT
<213> Hepatitis E Virus

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<220>  
 <223> plorf3-12.pep

<400> 204  
 Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys  
 1 5 10 15  
 Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys  
 20 25 30  
 Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala  
 35 40 45  
 Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser  
 50 55 60  
 Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met  
 65 70 75 80  
 Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala  
 85 90 95  
 Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro  
 100 105 110  
 Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp  
 115 120 125  
 Asp Asp Asp Lys  
 130

<210> 205  
 <211> 48  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Primer orf23

<400> 205  
 ctcagcagtc ccatcagcac cgccgcgcag accaagctgg ggcagatc 48

<210> 206  
 <211> 459  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> CKSORF32M-3.pep

<400> 206  
 Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys  
 1 5 10 15  
 Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys  
 20 25 30  
 Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Val  
 35 40 45  
 Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser  
 50 55 60  
 Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met  
 65 70 75 80  
 Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala  
 85 90 95  
 Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro  
 100 105 110

Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Gly Ala Asp Gly  
 115 120 125  
 Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu  
 130 135 140  
 His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala  
 145 150 155 160  
 Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr  
 165 170 175  
 Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val  
 180 185 190  
 Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu  
 195 200 205  
 Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu  
 210 215 220  
 Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln  
 225 230 235 240  
 Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu  
 245 250 255  
 Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp  
 260 265 270  
 Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr  
 275 280 285  
 Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser  
 290 295 300  
 Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile  
 305 310 315 320  
 Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys Leu  
 325 330 335  
 Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr  
 340 345 350  
 Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His  
 355 360 365  
 Arg Val Ala Ile Ser Thr Tyr Thr Ser Leu Gly Ala Gly Pro Thr  
 370 375 380  
 Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val  
 385 390 395 400  
 Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp  
 405 410 415  
 Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln  
 420 425 430  
 Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr  
 435 440 445  
 Arg Glu Ser Asp Tyr Lys Asp Asp Asp Asp Lys  
 450 455

<210> 207  
 <211> 459  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> PLORF32M-14-5.pep

<400> 207

Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys  
 1 5 10 15  
 Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys

20	25	30	
Pro Arg His Arg Pro Ala Ser Arg	Leu Ala Ala Val Val	Gly Gly Val	
35	40	45	
Ala Ala Val Pro Ala Val Val	Ser Gly Val Thr	Gly Leu Ile Leu Ser	
50	55	60	
Pro Ser Pro Ser Pro Ile Phe Ile	Gln Pro Thr Pro Ser Pro	Pro Met	
65	70	75	80
Ser Phe His Asn Pro Gly	Leu Glu Leu Ala Leu Asp	Ser Arg Pro Ala	
85	90	95	
Pro Leu Ala Pro Leu Gly Val	Thr Ser Pro Ser Ala	Pro Pro Leu Pro	
100	105	110	
Pro Val Val Asp Leu Pro Gln	Leu Gly Leu Arg Arg	Gly Ala Asp Gly	
115	120	125	
Thr Ala Glu Leu Thr Thr	Ala Ala Thr Arg Phe	Met Lys Asp Leu	
130	135	140	
His Phe Ala Gly Thr Asn	Gly Val Gly Glu Val	Gly Arg Gly Ile Ala	
145	150	155	160
Leu Thr Leu Phe Asn Leu Ala Asp	Thr Leu Leu Gly Gly	Leu Pro Thr	
165	170	175	
Glu Leu Ile Ser Ser Ala Gly	Gly Gln Leu Phe Tyr	Ser Arg Pro Val	
180	185	190	
Val Ser Ala Asn Gly Glu	Pro Thr Val Lys Leu	Tyr Thr Ser Val Glu	
195	200	205	
Asn Ala Gln Gln Asp Lys	Gly Ile Thr Ile Pro	His Asp Ile Asp Leu	
210	215	220	
Gly Asp Ser Arg Val Val	Ile Gln Asp Tyr Asp	Asn Gln His Glu Gln	
225	230	235	240
Asp Arg Pro Thr Pro Ser	Pro Ala Pro Ser Arg	Pro Phe Ser Val Leu	
245	250	255	
Arg Ala Asn Asp Val Leu	Trp Leu Ser Leu Thr	Ala Ala Glu Tyr Asp	
260	265	270	
Gln Thr Thr Tyr Gly Ser	Ser Thr Asn Pro Met	Tyr Val Ser Asp Thr	
275	280	285	
Val Thr Leu Val Asn Val	Ala Thr Gly Ala Gln	Ala Val Ala Arg Ser	
290	295	300	
Leu Asp Trp Ser Lys Val	Thr Leu Asp Gly Arg	Pro Leu Thr Thr Ile	
305	310	315	320
Gln Gln Tyr Ser Lys Thr	Phe Tyr Val Leu Pro	Leu Arg Gly Lys Leu	
325	330	335	
Ser Phe Trp Glu Ala Gly	Thr Thr Lys Ala Gly	Tyr Pro Tyr Asn Tyr	
340	345	350	
Asn Thr Thr Ala Ser Asp	Gln Ile Leu Ile	Glu Asn Ala Ala Gly His	
355	360	365	
Arg Val Ala Ile Ser Thr	Tyr Thr Ser Leu	Gly Ala Gly Pro Thr	
370	375	380	
Ser Ile Ser Ala Val Gly	Val Leu Ala Pro	His Ser Ala Leu Ala Val	
385	390	395	400
Leu Glu Asp Thr Ile Asp	Tyr Pro Ala Arg	Ala His Thr Phe Asp Asp	
405	410	415	
Phe Cys Pro Glu Cys Arg	Thr Leu Gly Leu	Gln Gly Cys Ala Phe Gln	
420	425	430	
Ser Thr Ile Ala Glu Leu	Gln Arg Leu Lys Met	Lys Val Gly Lys Thr	
435	440	445	
Arg Glu Ser Asp Tyr Lys	Asp Asp Asp Lys		
450	455		

<211> 36  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Primer orf2mid5p

<400> 208  
 tataatgatt catgggtgct gatgggactg ctgagc 36

<210> 209  
 <211> 418  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 1440o1.seq

<221> CDS  
 <222> (3) ... (416)

<223> Xaa = Unknown or Other at position 2  
 <223> Xaa = Unknown or Other at position 5  
 <223> Xaa = Unknown or Other at position 137

<400> 209  
 ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gcc aat 47  
 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn  
 1 5 10 15

tcc gcc ttg gcg aat gct gtg gtg gtt cg<sup>g</sup> ccg ttt tta tcc cgt gtt 95  
 Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val  
 20 25 30

caa act gat atc ctt att aac ctg atg caa ccc cgt cag ctt gtg ttc 143  
 Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe  
 35 40 45

cg<sup>g</sup> cct gaa gtt ctc tgg aac cat ccg atc cag cga gtt ata cat aat 191  
 Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn  
 50 55 60

gag ctg gaa caa tac tgt cga gcc cgc gct ggc cgc tgt ctt gag gtg 239  
 Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val  
 65 70 75

ggc gct cac cca agg tct att aat gat aac ccc aat gtt ctg cac ccg 287  
 Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg  
 80 85 90 95

tgc ttt ctc cgc ccg gtt ggg aga gac gtc cag cgc tgg tat tcc gcc 335  
 Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala  
 100 105 110

ccc act cgt ggt cca gcg gct aac tgc cgc cgt tct gcg cta cgc ggt 383

Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly  
 115 120 125

ttg ccc cct gtc gac cgc act tac tgt yty gat gg 418  
 Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp  
 130 135

<210> 210  
 <211> 138  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 2  
 <223> Xaa = Unknown or Other at position 5  
 <223> Xaa = Unknown or Other at position 137

<400> 210  
 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn Ser  
 1 5 10 15  
 Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln  
 20 25 30  
 Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg  
 35 40 45  
 Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu  
 50 55 60  
 Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly  
 65 70 75 80  
 Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys  
 85 90 95  
 Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro  
 100 105 110  
 Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu  
 115 120 125  
 Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp  
 130 135

<210> 211  
 <211> 197  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 1440o2.seq

<221> CDS  
 <222> (2)...(196)

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 211  
 g aca gaa ttr att tcg tcg gct gga ggt caa ctg ttc tac tcc cgc ccg 49  
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
 1 5 10 15  
  
 gtt gtc tca gcc aat ggc gag ccg act gtt aag tta tac acc tct gtc 97  
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 20 25 30  
  
 gag aat gca cag cag gat aag ggc att gct ata cca cat gat ata gac 145  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 35 40 45  
  
 tta ggg gat tcc cgt gtg gtt ata caa gat tat gay aac car cay gaa 193  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
 50 55 60  
  
 caa g 197  
 Gln  
 65

<210> 212  
 <211> 65  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 212  
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro 49  
 1 5 10 15  
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 20 25 30  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 35 40 45  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
 50 55 60  
 Gln  
 65

<210> 213  
 <211> 418  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 2015-1.seq

<221> CDS  
 <222> (3) ... (416)

<223> Xaa = Unknown or Other at position 2  
 <223> Xaa = Unknown or Other at position 5  
 <223> Xaa = Unknown or Other at position 137  
 <400> 213

ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gct aac	47
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn	
1 5 10 15	
tct gcc ttg gcg aat gct gtg gtc cg <sup>g</sup> cc <sup>g</sup> ttc ctg tcc cg <sup>c</sup> act	95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr	
20 25 30	
cag act gat att ctt att aat ttg atg caa ccc cg <sup>g</sup> caa ctt gta ttc	143
Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cg <sup>c</sup> cct gag gtt ttg tgg aac cat cc <sup>g</sup> atc cag cg <sup>a</sup> gtc ata cat aat	191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gag ctg gag cag tat tgc cgt gct gct ggt cg <sup>c</sup> tgc ctg gag gtt	239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75	
gg <sup>g</sup> gct cat cca aga tct atc aat gac aac cct aat gtt ctg cac cg <sup>g</sup>	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
80 85 90 95	
tgt ttc ctc cgt cc <sup>g</sup> gtt ggg cg <sup>a</sup> gac gta cag cgt tgg tat tct gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
cct act cg <sup>c</sup> ggc cc <sup>g</sup> gcg gct aat tgc cg <sup>c</sup> cgt tcc cg <sup>c</sup> tta cgt gg <sup>c</sup>	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
cta cct cct gtc gac cg <sup>c</sup> act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	

<210> 214  
 <211> 138  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 2  
 <223> Xaa = Unknown or Other at position 5  
 <223> Xaa = Unknown or Other at position 137  
 <400> 214

Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser  
 1 5 10 15  
 Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr Gln  
 20 25 30  
 Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg  
 35 40 45  
 Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu  
 50 55 60  
 Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly  
 65 70 75 80  
 Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys  
 85 90 95  
 Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro  
 100 105 110  
 Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu  
 115 120 125  
 Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp  
 130 135

&lt;210&gt; 215

&lt;211&gt; 197

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; 2015o2.seq

&lt;221&gt; CDS

&lt;222&gt; (2) ... (196)

&lt;223&gt; Xaa = Unknown or Other at position 3

&lt;223&gt; Xaa = Unknown or Other at position 60

&lt;223&gt; Xaa = Unknown or Other at positions 62-63

&lt;400&gt; 215

g aca gaa ttr att tcg tcg gct gga ggc cag ctc ttc tac tcc cgc cca  
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
 1 5 10 15

49

gtc gtc tca gcc aat ggc gag ccg act gtt aaa ttg tat aca tcc gtc  
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 20 25 30

97

gag aat gcg cag cag gac aag ggc att gcc ata cca cat gat ata gat  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 35 40 45

145

cta gga gat tcc cgc gtg gtt atc cag gat tat gay aac car cay gaa  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
 50 55 60

193

caa g  
 Gln  
 65

197

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<210> 216
<211> 65
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 216
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
1 5 10 15
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
20 25 30
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
35 40 45
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
50 55 60
Gln
65

<210> 217
<211> 251
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 14404-2.seq

<221> CDS
<222> (3)...(251)
<223> orf2

<223> orf3 from position 1 to position 165

<400> 217
at att cat cca acc aac ccc ttt gcc tcc gac gtc gta tcg caa tcc 47
Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser
1 5 10 15

ggg gct gga gct cgc cct cga cag ccg gcc cgc ccc ctc ggc tcc tct 95
Gly Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser
20 25 30

tgg cgt gac cag tcc cag cgc ccc gct gtc ccc cgt cgt cga tct 143
Trp Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Arg Ser
35 40 45

acc cca act ggg gct gcg ccg cta act gct gtt tca cca gcg cct gat 191
Thr Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp
50 55 60

acg gcc cca gtc cct gat gtt gac tct cgt ggc gct atc ttg cgc cgg 239

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Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg  
 65 70 75

cag tat aac cta 251  
 Gln Tyr Asn Leu  
 80

<210> 218  
 <211> 83  
 <212> PRT  
 <213> Hepatitis E Virus

<400> 218  
 Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser Gly  
 1 5 10 15  
 Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser Trp  
 20 25 30  
 Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Arg Ser Thr  
 35 40 45  
 Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr  
 50 55 60  
 Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln  
 65 70 75 80  
 Tyr Asn Leu

<210> 219  
 <211> 55  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> 14404-2.seq orf3

<400> 219  
 Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr Arg Asn Pro  
 1 5 10 15  
 Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu  
 20 25 30  
 Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Ser Pro Val Val Asp Leu  
 35 40 45  
 Pro Gln Leu Gly Leu Arg Arg  
 50 55

<210> 220  
 <211> 251  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 20154-2.seq

<221> CDS  
 <222> (3)...(251)  
 <223> orf2

<223> orf3 from position 1 to position 165

<400> 220

at att cat cca acc aac ccc ttt gcc gcc gac gtc gta tca caa ccc	47
Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro	
1 5 10 15	
ggg gct gga gct cgc cct cga cag ccg ccc cgc ccc ctc ggc tcc tct	95
Gly Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser	
20 25 30	
tgg cgt gat cag tcc cag cgc ccc tcc gct gcc ccc cgt cgt cga tct	143
Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Arg Ser	
35 40 45	
acc cca gct ggg gct gcg ccg tta act gct gtt tcc cct gcg ccc gat	191
Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp	
50 55 60	
acg gcc cca gtc ccc gac gtt gat tcc cgt ggt gcc atc ctg cgc cgg	239
Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg	
65 70 75	
cag tat aac cta	251
Gln Tyr Asn Leu	
80	

<210> 221

<211> 83

<212> PRT

<213> Hepatitis E Virus

<400> 221

Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro Gly	
1 5 10 15	
Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser Trp	
20 25 30	
Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Ser Thr	
35 40 45	
Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr	
50 55 60	
Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln	
65 70 75 80	
Tyr Asn Leu	

<210> 222

<211> 55

<212> PRT

<213> Hepatitis E Virus

<220>

<223> 20154-2.seq orf3

<400> 222

Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr His Asn Pro	
---	--

1	5	10	15												
Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala	Pro	Ser	Ala	Pro	Leu
	20							25							30
Gly	Val	Ile	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro	Pro	Val	Val	Asp	Leu
	35							40							45
Pro	Gln	Leu	Gly	Leu	Arg	Arg									
	50							55							

<210> 223  
 <211> 48  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> US-2 3-2e

	<400> 223														
Thr	Ile	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1					5				10						15
Glu	Cys	Arg	Thr	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Ile
					20				25						30
Ala	Glu	Leu	Gln	Arg	Leu	Lys	Met	Lys	Val	Gly	Lys	Thr	Arg	Glu	Ser
					35				40						45

<210> 224  
 <211> 33  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> US-2 4-2

	<400> 224														
Asp	Ser	Arg	Pro	Ala	Pro	Leu	Val	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser
1					5				10						15
Ala	Pro	Pro	Leu	Pro	Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg
					20				25						30

Arg

<210> 225  
 <211> 450  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 5p.pile {hpesvp}

	<400> 225					
ggctcctggc	atcactactg	ctattgagca	ggctgctcta	gcagcggcca	actctgccct	60
ggcgaatgct	gtggtagtta	ggcctttct	ctctcaccag	cagattgaga	tcctcattaa	120
cctaatgcaa	cctcgccagc	ttgtttccg	ccccgagggtt	ttctggaatc	atccccatcca	180
gcgtgtcatc	cataacgagc	tggagctta	ctgcccgcgc	cgctccggcc	gctgtcttga	240
aattggcgcc	catccccgct	caataaatga	taatcctaatt	gtgtccacc	gctgcttcct	300
ccgcccgttt	ggcggtgatg	ttcagcgctg	gtatactgct	cccactcgcg	ggccggctgc	360
taattgccgg	cgttccgcgc	tgcgcgggct	tcccgtgct	gaccgcactt	actgcctcga	420
cgggtttct	ggctgtaact	ttcccgccga				450

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<210> 226
<211> 450
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 5p.pile {hpeuigh}

<400> 226
ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca attctgccct      60
tgcgaatgct gtggtagtta ggcctttct ctctcaccag cagattgaga tccttattaa      120
cctaattgcaaa cctcgccagc ttgtttccg ccccgagggtt ttctggacc accccatcca      180
gcgtgtcatc cataatgagc tggagcttta ctgtcgcccg cgctccggcc gctgccttga      240
aattggtgcc caccctcgct caataaacga caatcctaattt gtggtccacc gctgcttcct      300
ccgcccgtcc gggcgtgatg ttcaagcggtt gtataactgct cctaccccgcg ggccggctgc      360
taattggccgg ggttccgcac tgcgccggct ccccgctgct gaccgcactt actgcttcga      420
cggttttctt ggctgttaact ttcccgccga      450

<210> 227
<211> 450
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 5p.pile {hpea}

<400> 227
ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca actctgccct      60
tgcgaatgct gtggtagtta ggcctttct ctctcaccag cagattgaga tccttattaa      120
cctaattgcaaa cctcgccagc ttgtttccg ccccgagggtt ttctggacc accccatcca      180
gcgtgttatac cataatgagc tggagcttta ctgtcgcccg cgctccggcc gctgcctcga      240
aattggtgcc caccctcgct caataaatga caatcctaattt gtggtccacc gttgcttcct      300
ccgtcctggcc gggcgtgatg ttcaagcggtt gtataactgccc cctaccccgcg ggccggctgc      360
taattggccgg ggttccgcac tgcgccggct ccccgctgct gaccgcactt actgcttcga      420
cggttttctt ggctgttaact ttcccgccga      450

<210> 228
<211> 446
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 5p.pile {840455p}

<400> 228
cctggcatta ctactgccat tgagcaggct gctctggctg cggccaattt tgccttggcg      60
aatgctgtgg tggttcggcc gttttatct cgcgtgcaaa ccgagattct tattaatttg      120
atgcaacccc ggcagttggt tttccggccct gaggtactttt ggaatcaccc tatccagcgg      180
gttataacata atgaattaga acagtactgc cgggctcggtt ctggtcgttgc cttggagggtt      240
ggagctcacc caagatccat taatgacaac cccaaacgttc tgcatcggtt tttcctttaga      300
ccggttggcc gagatgttca ggcgttggct tctggccccc cccgcggccc tgcggctaat      360
tgcggccgct ccgcgttgcg tggctccccc cccgctgacc gcacttactg ctttgatgga      420
ttctcccggtt gtgttttgc tgcaga      446

<210> 229
<211> 450

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<212> DNA
<213> Hepatitis E Virus

<220>
<223> 5p.pile {hopenssp}

<400> 229
ggctcctggc attactactg ctattgagca agcagctcta gcagcggcca actccgccc 60
tgcgaatgct gtgggtgtcc ggccttcct ttccatcatcag cagttgaga tccttataaa 120
tctcatcaa cctcggcagc tgggtttcg tcctgagggt ttttggaaatc acccgattca 180
acgtgttata cataatgagc ttgagcagta ttgccgtgtcg cgctcgggtc gtcgccttga 240
gattggagcc caccacgct ccattaatga taatcctaatttgc gtcctccatc gtcgccttct 300
ccaccccggtc ggcggggatgt ttcagcgctg gtacacagcc cgcactaggg gacctgcggc 360
gaactgtcgc cgctcggcac ttctgggtct gccaccagcc gaccgcactt actgtttga 420
tggcttgcc ggctgcccgtt ttgcggccga 450

<210> 230
<211> 450
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 5p Consensus

<221> variation
<222> (1)...(450)
<223> n = a or g or c or t/u, unknown or other in each
      instance and is indicated in Figure 9

<400> 230
nnnnccctggc atnactactg cnattgagca ngcngctctn gcngcggcca antcngccnt 60
ngcgaatgct gtggtngnnnn ggccttntnt ntcncnnnnnng cannnngaga tnctnatnaa 120
nntnatcaa ccncgncagn tngtnntncg nccngaggtn ntntgaaanc anccnatnca 180
ncgngtnatn cataangann tngancnnta ntgncngncn cgnncnggnc gntgnntnga 240
nnttggngcn canccnnngnt cnatnaanga naancnaan gtnntncanc gntgnntnct 300
nnnnccngnn ggnccngatgt ttcagcgntg gtanncngcn cchnacnngng gnccngcngc 360
naantgnccn ngntcngcn tncngngnct nccnnngcn gaccgcactt actgnntnga 420
nggnntnnccn ngntgnnnnnt ttncngcnga 450

<210> 231
<211> 300
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 3p.pile {hpea} shown in Figure 9B

<400> 231
actgagtcag tgaaggccagt gcttgacctg acaaattcaa ttctgtgtcg ggtggaatga 60
ataacatgtc ttttgcgtcg cccatgggtt cgcgaccatg cgccctcgcc ctatttgtct 120
gttgcgtcttc atgtttctgc ctatgcgtcc cgccaccgg cccggtcagc cgtctggccg 180
ccgtcggtgg cggcgcagcg gcggttccgg cggtggttcc tgggttgacc gggttgattc 240
tcagcccttc gcaatcccctt atattcatcc aaccaacccc ttgcggcccg atgtcaccgc 300

<210> 232
<211> 300
<212> DNA

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<213> Hepatitis E Virus  
 <220>  
 <223> 3p.pile {hpeuigh} shown in Figure 9B  
 <400> 232  
 actgagtcgg tgaagccagt gctcgacttg acaaattcaa tcctgtgtcg ggtggaatga 60  
 ataacatgtc ttttgcgtcg cccatgggtt ggcgaccatg cgcgcctcgcc ctatttgct 120  
 gttgctcctc atgtttctgc ctatcggtcc cgcgcacccg cccggtcagc cgtctggccg 180  
 ccgtcggtgg cggcgccagcg gcggttccgg cgggtgttcc tgggtgtacc gggttgattc 240  
 tcagcccttc gcaatcccct atattcatcc aaccaacccc ttgcggcccg atgtcacccgc 300

<210> 233  
 <211> 300  
 <212> DNA  
 <213> Hepatitis E Virus  
 <220>  
 <223> 3p.pile {hpesvp} shown in Figure 9B  
 <400> 233  
 actgagtcag taaaaccagt gctcgacttg acaaattcaa tcttgcgtcg ggtggaatga 60  
 ataacatgtc ttttgcgtcg cccatgggtt ggcgaccatg cgcgcctcgcc ctatttgtt 120  
 gctgctcctc atgttttgc ctatcggtcc cgcgcacccg cccggtcagc cgtctggccg 180  
 ccgtcggtgg cggcgccagcg gcggttccgg cgggtgttcc tgggtgtacc gggttgattc 240  
 tcagcccttc gcaatcccct atattcatcc aaccaacccc ttgcggcccg atgtcacccgc 300

<210> 234  
 <211> 300  
 <212> DNA  
 <213> Hepatitis E Virus  
 <220>  
 <223> 3p.pile {hpenssp} shown in Figure 9B  
 <400> 234  
 acagagtcgt ttaagcctat acttgacctt acacactcaa ttatgcacccg gtctgaatga 60  
 ataacatgtg gtttgcgtcg cccatgggtt cgccaccatg cgcgccttaggc ctctttgct 120  
 gttgttcctc ttgtttctgc ctatgttgc cgcgcacccg accggtcagc cgtctggccg 180  
 ccgtcggtgg cggcgccagcg gcggttccgg cgggtgttcc tgggtgtacc gggttgattc 240  
 tcagcccttc gcaatcccct atattcatcc aaccaacccc ttgcggcccg acgttgcgc 300

<210> 235  
 <211> 297  
 <212> DNA  
 <213> Hepatitis E Virus  
 <220>  
 <223> 3p.pile {840453p} shown in Figure 9B  
 <400> 235  
 acagagacta ttaaacctgt acttgatctc acaaattcca tcatacagcg ggtggaatga 60  
 ataacatgtc ttttgcgtcg cccatgggtt caccatgcgc cctagggtcg ttctgttgc 120  
 gttcctcatg ttctgccta tgctgcccgc gccaccggcc ggtcagccgt ctggccgtcg 180  
 ccgtggccgg cgccagccgg gtcggccgg tgggttctgg agtacagagg ttgattctca 240  
 gcccctcgcc ctccctata ttcatccaac caaccccttc gccgcccgtg tcgtttc 297

<210> 236  
 <211> 300  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p Consensus shown in Figure 9B

<221> variation  
 <222> (3)...(300)  
 <223> n = a or g or c or t/u, unknown or other in each  
 instance and is indicated in Figure 9B

<400> 236

acngagncnn tnaanccnn nctnganntn acanantcna tnnnlnnnncg gnnngaatga	60
ataacatgtm ntgtgcnnncg cccatgggnt nnnnaccatg cgccctnggn ctntntgnt	120
gntgntcctc ntgttntgc ctatnntgcc cgccgcaccc nccggtcagc cgtctggccg	180
ncgncgtggg cggcgcagcg gcggtncggg cggtggttc tggngtgacn gggttgattc	240
tcagcccttc gcnntccct atattcatcc aaccaacccc ttngccncng angtnnnnnnc	300

<210> 237  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpea} shown in Figure 9C

<400> 237

agcgcttacc ctgttaacc ttgctgacac cctgcttggc ggtctaccga cagaattgat	60
ttcgctggct ggtggccagc tgtttactc tcgccccgtc gtctcagcca atggcgagcc	120
gactgttaag ctgtatacat ctgtggagaa tgctcagcag gataagggttta ttgcaatccc	180
gcatgacatc gacctcgggg aatccgtgt agttattcag gattatgaca accaacatga	240
gcaggaccga	250

<210> 238  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpeuigh} shown in Figure 9C

<400> 238

agcgcttacc ctgttaacc ttgctgacac cctgcttggc ggtctaccga cagaattgat	60
ttcgctggct ggtggccagc tgtttactc tcgccccgtc gtctcagcca atggcgagcc	120
gactgttaag ctgtatacat ctgttagagaa tgctcagcag gataagggttta ttgcaatccc	180
gcatgacatc gacctcgggg aatctcgagt tgttattcag gattatgaca accaacatga	240
gcaggaccgg	250

<210> 239  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpesvp} shown in Figure 9C

<400> 239  
 agccctcacc ctgttcaacc ttgctgacac tctgcttggc ggcctgccga cagaattgat 60  
 ttcgtcggt ggtggccagc tgtttactc ccgtcccgtt gtctcagcca atggcgagcc 120  
 gactgttaag ttgtatacat ctgttagagaa tgctcagcag gataagggtt ttgcaatccc 180  
 gcatgacatt gacctcgag aatctcggtt gtttattcag gattatgata accaacatga 240  
 acaagatcg 250

<210> 240  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpenssp} shown in Figure 9C

<400> 240  
 agctctaaca ttacttaacc ttgctgacac gtcctcggc gggctcccgaa cagaattaaat 60  
 ttcgtcggt ggcgggcaac tgtttattc ccgcccggtt gtctcagcca atggcgagcc 120  
 aaccgtgaaat ctctatacat cagtgagaa tgctcagcag gataagggtt ttgctatccc 180  
 ccacgatac gatcttgggtt attcgcgtgt ggtcattcag gattatgaca accagcatga 240  
 gcaggatcg 250

<210> 241  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {840453p} shown in Figure 9C

<400> 241  
 tgccctgact ctgtttaatc ttgctgatac gtttcttgggt gtttaccga cagaattgat 60  
 ttcgtcggt gggggtaac tgtttactc ccgcctgtt cagaattgat ttcgtcggt 120  
 gggggtaac tgtttactc ccgcctgtt tgccgacaa gacaagggtt tcaccattcc 180  
 acacgacata gatttaggtt actcccggtt gtttattccag gattatgata accagcacga 240  
 acaagatcg 250

<210> 242  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p Consensus shown in Figure 9C

<221> variation  
 <222> (1)...(250)  
 <223> n = a or g or c or t/u, unknown or other at each  
 instance and is indicated in Figure 9C

<400> 242  
 ngnctnacn ntntnaanc ttgctganac nctnctnggn ggnntnccga cagaattnat 60  
 ttcgtcggt ggnngncanc tgtttantic ngnccngtn gtctcngcca atggcgagcc 120  
 nacngtnaag ntntanacat cngtngagaa tgcnccagcan ganaagggnn tnnncnatncc 180  
 ncanganatn ganntngng antncngnt ngtnatnccag gattatgana accancanga 240  
 ncangqancqn 250

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<210> 243
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Aulol-wlabolp1.pat

<221> CDS
<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2
<223> Xaa = Unknown or Other at position 5
<223> Xaa = Unknown or Other at position 137

<400> 243
ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aat      47
  Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
    1           5           10          15

tct gcc ttg gcg aat gct gtg gtt cgg ccg ttt tta tcc cgt gtg      95
  Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
    20          25          30

cag act gag atc ctt att aac ttg atg caa cct cgg cag ctg gtg ttc      143
  Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
    35          40          45

cga cct gag gtg ctt tgg aat cat ccc att cag cgg gtt atc cat aat      191
  Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
    50          55          60

gag tta gaa caa tac tgc cgg gcc cgg ggc cgt tgc cta gag gtg      239
  Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
    65          70          75

ggg gcc cac cca agg tcc att aac gat aac ccc aat gtt ttg cac cgg      287
  Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
    80          85          90          95

tgt ttt ctg cga ccg gtc ggg agg gat gtt cag cgg tgg tac tct gcc      335
  Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
    100         105         110

ccc acc cgc ggc cct gcg gct aac tgc cgg cgc tcc gct ttg cgt ggc      383
  Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
    115         120         125

ctt ccc ccc gtc gac cgc act tac tgt yty gat gg      418
  Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
    130         135

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<211> 138
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 244
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn Ser
 1           5           10          15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
 20          25          30
Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg
 35          40          45
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
 50          55          60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
 65          70          75          80
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
 85          90          95
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
100         105         110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
115         120         125
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
130         135

<210> 245
<211> 197
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Aul02-wlao2.pat

<221> CDS
<222> (2)...(196)

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 17

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 245
g aca gaa ttr att tcg tcg gct ggg gga cag tta ttc tac tcc cgc cct      49
  Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
  1           5           10          15

gtt gtc tca gcc aat ggc gag ccg act gtt aaa tta tat aca tct gta      97
  Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val

```

20

25

30

gag aat gcg cag cag gac aag ggg att gcc atc cca cat gat ata gat 145  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 35 40 45

ctg ggc gac tct cgt gtg atc cag gat tat gay aac car cay gaa 193  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
 50 55 60

caa g 197  
 Gln  
 65

<210> 246  
 <211> 65  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 17

<223> xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 246  
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro.  
 1 5 10 15  
 Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 20 25 30  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 35 40 45  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
 50 55 60

Gln  
 65

<210> 247  
 <211> 418  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Ar1o1-f73o1p1.pat

<221> CDS  
 <222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<pre> &lt;400&gt; 247 ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aac Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn 1           5           10          15 </pre> <pre> tct gcc ttg gcg aat gct gtg gtg gtt cg<sup>g</sup> ccg ttt tta tcc cgt gtg Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val 20          25          30 </pre> <pre> cag acc gag att ctt att aac cta atg caa ccc cg<sup>g</sup> cag ctg gtt ttt Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe 35          40          45 </pre> <pre> cgt cct gag gtg ctt tgg aac cat cct atc cag cg<sup>g</sup> gtt att cat aat Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn 50          55          60 </pre> <pre> gag tta gaa cag tac tgt cg<sup>g</sup> gct cg<sup>g</sup> gct ggt cgc tgc cta gag gtc Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val 65          70          75 </pre> <pre> ggg gcc cac cca agg tcc att aat gat aac cct aat gtt ttg cac cg<sup>g</sup> Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg 80          85          90          95 </pre> <pre> tgc ttc cta cga cca gtc ggg agg gat gtt caa cgt tgg tat tcc gcc Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala 100         105         110 </pre> <pre> ccc acc cgc ggt cct gct gcc aac tgc cgc cgt tcc gct ctg cgc ggc Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly 115         120         125 </pre> <pre> ctc cct ccc gtc gac cgc act tac tgt yty gat gg Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp 130         135 </pre>	47  95  143  191  239  287  335  383  418
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<210> 248
<211> 138
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 248
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
1           5           10          15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
20          25          30
Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg

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35	40	45
Pro Glu Val Leu Trp Asn His	Pro Ile Gln Arg Val	Ile His Asn Glu
50	55	60
Leu Glu Gln Tyr Cys Arg Ala Arg	Ala Gly Arg Cys	Leu Glu Val Gly
65	70	75
Ala His Pro Arg Ser Ile Asn Asp	Asn Pro Asn Val	Leu His Arg Cys
85	90	95
Phe Leu Arg Pro Val Gly Arg Asp	Val Gln Arg Trp	Tyr Ser Ala Pro
100	105	110
Thr Arg Gly Pro Ala Ala Asn Cys	Arg Arg Ser Ala	Leu Arg Gly Leu
115	120	125
Pro Pro Val Asp Arg Thr Tyr	Cys Xaa Asp	
130	135	

<210> 249  
 <211> 145  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Ar1-f73o2p2.pat

<221> CDS  
 <222> (1) ... (144)

<223> Xaa = Unknown or Other at position 1

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 44

<223> Xaa = Unknown or Other at positions 46-47

400	49													
gt	tc	g	cc	aa	gg	cc	aa	tt	aa	cc	tt	gt		
Xaa	Val	Xaa	Ala	Asn	Gly	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val
1			5				10					15		48

gag	aa	gc	ca	ca	ga	aa	gg	at	cc	ca	ca	ga	at	ga	49
Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His	Asp	Ile	Asp
20							25					30			96

ctg	gg	ga	tcc	cgt	gt	tc	at	cag	ga	ta	ga	aa	ca	ca	ga	144
Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Xaa	Asn	Xaa	Xaa	Glu	
35							40				45					

c 145

<210> 250  
 <211> 48  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 1  
 <223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 44  
 <223> Xaa = Unknown or Other at positions 46-47  
 <400> 250  
 Xaa Val Xaa Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 1 5 10 15  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 20 25 30  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
 35 40 45

<210> 251  
 <211> 418  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Ar2o1-f77o1p1.pat

<221> CDS  
 <222> (3) ... (416)

<223> Xaa = Unknown or Other at position 2  
 <223> Xaa = Unknown or Other at position 5  
 <223> Xaa = Unknown or Other at position 41  
 <223> Xaa = Unknown or Other at position 44  
 <223> Xaa = Unknown or Other at position 93  
 <223> Xaa = Unknown or Other at position 137

<400> 251  
 ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gct aac 47  
 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn  
 1 5 10 15

tct gcc ttg gcg aat gct gtg gtg gtt cg<sup>g</sup> ccg ttt cta tcc cgt gtg 95  
 Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val  
 20 25 30

cag act gag atc ctt att aac tta atg car ccc cg<sup>g</sup> car ctg gtt ttc 143  
 Gln Thr Glu Ile Leu Ile Asn Leu Met Xaa Pro Arg Xaa Leu Val Phe  
 35 40 45

cgt ccc gag gtg ctt tgg aat cat ccc att caa cg<sup>g</sup> gtt att cat aat 191  
 Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn  
 50 55 60

gaa tta gag cag tac tgc cg<sup>g</sup> acc cg<sup>g</sup> gct ggc cgt tgt tta gag gtc 239  
 Glu Leu Glu Gln Tyr Cys Arg Thr Arg Ala Gly Arg Cys Leu Glu Val  
 65 70 75

gga gcc cat cca agg tcc att aat gac aac cct aac gtt cyg cac cg	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Xaa His Arg	
80 85 90 95	
tgc ttc tta cga cca gtc ggg agg gat gtc caa cga tgg tac tca gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc act cgc ggc cct gcg gct aat tgc cgt cgt tcc gct ttg cgt ggt	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc cct cct gtc gac cgc act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	
<210> 252	
<211> 138	
<212> PRT	
<213> Hepatitis E Virus	
<220>	
<223> Xaa = Unknown or Other at position 2	
<223> Xaa = Unknown or Other at position 5	
<223> Xaa = Unknown or Other at position 41	
<223> Xaa = Unknown or Other at position 44	
<223> Xaa = Unknown or Other at position 93	
<223> Xaa = Unknown or Other at position 137	
<400> 252	
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn Ser	
1 5 10 15	
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln	
20 25 30	
Thr Glu Ile Leu Ile Asn Leu Met Xaa Pro Arg Xaa Leu Val Phe Arg	
35 40 45	
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu	
50 55 60	
Leu Glu Gln Tyr Cys Arg Thr Arg Ala Gly Arg Cys Leu Glu Val Gly	
65 70 75 80	
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Xaa His Arg Cys	
85 90 95	
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro	
100 105 110	
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu	
115 120 125	
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	
<210> 253	
<211> 197	

<212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Ar2o2-f7702.pat

<221> CDS  
 <222> (2)...(196)

<223> Xaa = Unknown or Other at position 3  
 <223> Xaa = Unknown or Other at position 60  
 <223> Xaa = Unknown or Other at positions 62-63

<400> 253

g aca gaa ttr att tcg tcg gct ggg ggt cag ttg ttt tac tcc cgc cct	49
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro	
1 5 10 15	
gtc gtc tca gcc aat ggc gag ccg act gtt aag ttg tat aca tct gtg	97
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val	
20 25 30	
gag aat gcg cag cag gat aaa gga atc gcc atc cca cac gac ata gat	145
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp	
35 40 45	
ctg ggc gat tcc cgt gtg gtt att cag gat tat gay aac car cay gaa	193
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu	
50 55 60	
caa g	197
Gln	
65	

<210> 254  
 <211> 65  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 3  
 <223> Xaa = Unknown or Other at position 60  
 <223> Xaa = Unknown or Other at positions 62-63

<400> 254

Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro	
1 5 10 15	
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val	
20 25 30	
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp	
35 40 45	
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu	

50	55	60	
Gln			
65			
<pre> &lt;210&gt; 255 &lt;211&gt; 23 &lt;212&gt; DNA &lt;213&gt; Hepatitis E Virus </pre>			
<pre> &lt;220&gt; &lt;223&gt; HEVConsORF 1N-a1 </pre>			
<pre> &lt;400&gt; 255 ccrtcarrc artaggtgcg gtc </pre>			
<pre> &lt;210&gt; 256 &lt;211&gt; 25 &lt;212&gt; DNA &lt;213&gt; Hepatitis E Virus </pre>			
<pre> &lt;220&gt; &lt;223&gt; HEVConsORF 2N-a1 </pre>			
<pre> &lt;400&gt; 256 cytggytcrtg ytgggttgtca taatc </pre>			
<pre> &lt;210&gt; 257 &lt;211&gt; 21 &lt;212&gt; DNA &lt;213&gt; Hepatitis E Virus </pre>			
<pre> &lt;220&gt; &lt;223&gt; HEVConsORF 1N-s2 </pre>			
<pre> &lt;400&gt; 257 cygccccytkgc gaatgctgtg g </pre>			
<pre> &lt;210&gt; 258 &lt;211&gt; 25 &lt;212&gt; DNA &lt;213&gt; Hepatitis E Virus </pre>			
<pre> &lt;220&gt; &lt;223&gt; HEVConsORF 2N-a2 </pre>			
<pre> &lt;400&gt; 258 gytcrtgytg rttrtcataa tcctg </pre>			